

SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 75
TYPE: DNA
ORGANISM: artificial
FEATURE: OTHER INFORMATION: Primer for bacteria
-11-088-257-1

Query Match 74.8%; Score 31.4; DB 7; Length 75;
Best Local Similarity 85.4%; Pred. No. 0.00931;
Matches 35; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

RESULT 3
US-10-933-025-24
Sequence 24, Application US/10933025
Publication No. US20050265987A1
GENERAL INFORMATION:
APPLICANT: ROSEN, STEVEN
APPLICANT: HEMMERICH, STEFAN
APPLICANT: TOMITA, MEGUMI
TITLE OF INVENTION: Sulfotransferases and methods of use
FILE REFERENCE: UCAL-230CON
CURRENT APPLICATION NUMBER: US/10/933, 025
CURRENT FILING DATE: 2004-09-01
PRIOR APPLICATION NUMBER: 10/025, 966
PRIOR FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/258, 577
PRIOR FILING DATE: 2000-12-27
PRIOR APPLICATION NUMBER: 60/267, 831
PRIOR FILING DATE: 2001-09-02
NUMBER OF SEQ ID NOS: 26
SEQ ID NO 24
LENGTH: 171936
TYPE: DNA
ORGANISM: Mus musculus
-10-933-025-24

Query Match 57.1%; Score 24; DB 6; Length 171936;
Best Local Similarity 75.0%; Pred. No. 3.4;
Matches 30; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

RESULT 4
US-11-088-257-10
Sequence 10, Application US/11088257
Publication No. US20050260636A1
GENERAL INFORMATION:
APPLICANT: CELLEX INC
TITLE OF INVENTION: Methods for Detection of Biological Organisms Using tRNA
FILE REFERENCE: CELLEX-0006
CURRENT APPLICATION NUMBER: US/11/088, 257
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: US 60/555, 683
PRIOR FILING DATE: 2004-03-24
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 10
LENGTH: 25

Query Match 55.7%; Score 23.4; DB 7; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 AAGCTCGTGTCTACCAACTGAGT 34
Db 1 AAGCTCGTGTCTACCAACTGAGT 25

OTHER INFORMATION: Methods For Detection of Biological Organisms Using tRNA
US-11-088-257-10

Query Match 55.7%; Score 23.4; DB 7; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 AAGCTCGTGTCTACCAACTGAGT 34
Db 1 AAGCTCGTGTCTACCAACTGAGT 25

RESULT 5
US-11-088-257-30
Sequence 30, Application US/11088257
Publication No. US20050260636A1
GENERAL INFORMATION:
APPLICANT: CELLEX INC
TITLE OF INVENTION: Methods For Detection of Biological Organisms Using tRNA
FILE REFERENCE: CELLEX-0006
CURRENT APPLICATION NUMBER: US/11/088, 257
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: US 60/555, 683
PRIOR FILING DATE: 2004-03-24
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.2
SEQ ID NO 30
LENGTH: 25
TYPE: DNA
ORGANISM: artificial
FEATURE: OTHER INFORMATION: Primer for bacteria
US-11-088-257-30

Query Match 55.7%; Score 23.4; DB 7; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.3;
Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 10 AAGCTCGTGTCTACCAACTGAGT 34
Db 1 AAGCTCGTGTCTACCAACTGAGT 25

RESULT 6
US-10-750-185-31677/C
Sequence 31677, Application US/10750185
Publication No. US20050260630A1
GENERAL INFORMATION:
APPLICANT: MMI GENOMICS, INC.
APPLICANT: DENISE, Sue K.
APPLICANT: KERR, Richard
APPLICANT: ROSENFIELD, David
APPLICANT: HOLM, Tom
APPLICANT: BATES, Stephen
APPLICANT: FANTIN, Dennis
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
FILE REFERENCE: MM110-2
CURRENT APPLICATION NUMBER: US/10/750, 185
CURRENT FILING DATE: 2003-12-31
PRIOR APPLICATION NUMBER: US 60/437, 482
PRIOR FILING DATE: 2002-12-31
NUMBER OF SEQ ID NOS: 64322
SOFTWARE: PatentIn version 3.1
SEQ ID NO 31677
LENGTH: 5071
TYPE: DNA
ORGANISM: Bovine 19866880454815

Query Match 54.8%; Score 23; DB 6; Length 5071;
Best Local Similarity 74.4%; Pred. No. 4.7%;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SEQ ID NO 10
LENGTH: 25

TYPE: DNA
ORGANISM: artificial
FEATURE:

Qy 3 GCTTGGAAAGCTGGCTCTAACACTGAGTACCAACCG 41
 Db 1391 GATTGCAAGGGATTCTAACACTGAGTACACAG 1353

RESULT 7

US-10-750-623-31677/c
 ; Sequence 31677, Application US/10750623
 ; Publication No. US2005026753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENBLD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MMII1100-1
 ; CURRENT APPLICATION NUMBER: US/10/750,623
 ; CURRENT FILING DATE: 2003-12-31
 ; PRIORITY NUMBER: US 60/437,482
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIN version 3.1
 ; SEQ ID NO: 51268
 ; LENGTH: 1155
 ; TYPE: DNA
 ; ORGANISM: Bovine
 ; LENGTH: 5071
 ;
 ; ORGANISM: Bovine 19866880454815
 ; US-10-750-623-31677

Query Match 54 .8%; Score 23; DB 6; Length 5071;
 Best Local Similarity 74.4%; Pred. No. 4.7%;
 Matches 29; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy 3 GCTTGGAAAGCTGGCTCTAACACTGAGTACCAACCG 41.
 Db 1391 GATTGCAAGGGATTCTAACACTGAGTACACAG 1353

RESULT 9

US-10-750-623-51288
 ; Sequence 51288, Application US/10750623
 ; Publication No. US2005028751A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENBLD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MMII1100-1
 ; CURRENT APPLICATION NUMBER: US/10/750,623
 ; CURRENT FILING DATE: 2003-12-31
 ; PRIORITY NUMBER: US 60/437,482
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIN version 3.1
 ; SEQ ID NO: 51268
 ; LENGTH: 1155
 ; TYPE: DNA
 ; ORGANISM: Bovine
 ; LENGTH: 5071
 ;
 ; ORGANISM: Bovine 19866880733794
 ; US-10-750-623-51288

Query Match 54 .3%; Score 22.8; DB 6; Length 1155;
 Best Local Similarity 71.4%; Pred. No. 4.5%;
 Matches 30; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

Qy 1 GAGCTTGGAAAGCTGGCTCTAACACTGAGTACCAACCGC 41.
 Db 1037 GAGCATCTCAACTCTGTCATGCAACAGAAACCACTGC 1078

RESULT 10

US-10-750-185-45201
 ; Sequence 45201, Application US/10750185
 ; Publication No. US20050260503A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENBLD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MMII1100-2
 ; CURRENT APPLICATION NUMBER: US/10/750,185
 ; CURRENT FILING DATE: 2003-12-31
 ; PRIORITY NUMBER: US 60/437,482
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIN version 3.1
 ; SEQ ID NO: 45201
 ; LENGTH: 1155
 ; TYPE: DNA
 ; ORGANISM: Bovine
 ; LENGTH: 5071
 ;
 ; ORGANISM: Bovine 19866881206092
 ; US-10-750-185-45201

Query Match 53 .8%; Score 22.6; DB 6; Length 1171;
 Best Local Similarity 75.7%; Pred. No. 5.7%;
 Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 5 TTGGGAAGCTGGCTCTAACACTGAGTACCAACCG 41.
 Db 1601 TTGGCAAGGGTTTACAGCTGAGCCACACAG 1637

RESULT 11

US-10-750-623-45201 ; Sequence 45201; Application US/10750623
 ; Publication No. US20050508753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFIELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-1
 ; CURRENT APPLICATION NUMBER: US/10/750,623
 ; CURRENT FILING DATE: 2003-12-31
 ; PRIORITY NUMBER: US 60/437,482
 ; PRIORITY FILING DATE: 2003-12-31
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIN version 3.1
 ; SEQ ID NO: 45201
 ; LENGTH: 1717
 ; TYPE: DNA
 ; ORGANISM: Bovine 19866880468477
 ; US-10-750-623-45201
 Query Match 53.8%; Score 22.6; DB 6; Length 1717;
 Best Local Similarity 75.7%; Pred. No. 5; 7;
 Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 5 TTGGGAAGCTCTGCTTACCAACTGAGCTAACACCG 41
 Db 1601 TTGGCAGCGAAGTTCTTACCGCTGAGCCACACAG 1637
 RESULT 12 US-10-750-185-10822
 ; Sequence 10822; Application US/10750185
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFIELD, David
 ; APPLICANT: HOLM, Tom
 ; APPLICANT: BATES, Stephen
 ; APPLICANT: FANTIN, Dennis
 ; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
 ; FILE REFERENCE: MM1100-2
 ; CURRENT APPLICATION NUMBER: US/10/750,185
 ; CURRENT FILING DATE: 2003-12-31
 ; PRIORITY NUMBER: US 60/437,482
 ; PRIORITY FILING DATE: 2003-12-31
 ; NUMBER OF SEQ ID NOS: 64922
 ; SOFTWARE: PatentIN version 3.1
 ; SEQ ID NO: 30822
 ; LENGTH: 2652
 ; TYPE: DNA
 ; ORGANISM: Bovine 19866880468477
 ; US-10-750-185-10822
 Query Match 53.8%; Score 22.6; DB 6; Length 2652;
 Best Local Similarity 75.7%; Pred. No. 6.2;
 Matches 28; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
 Qy 5 TTGGGAAGCTCTGCTTACCAACTGAGCTAACACCG 41
 Db 1319 TTGGCAGGTGGTCCTACCCCTGAGCCACACAG 1355
 RESULT 13 US-10-750-623-30822
 ; Sequence 30822; Application US/10750623
 ; Publication No. US2005028753A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MMI GENOMICS, INC.
 ; APPLICANT: DENISE, Sue K.
 ; APPLICANT: KERR, Richard
 ; APPLICANT: ROSENFIELD, David

; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: PANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR IMPROVING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 6422
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 38017
; LENGTH: 2005
; TYPE: DNA
; ORGANISM: Bovine 19866880521244
; US-10-750-185-38017

Query Match 52.4%; Score 22; DB 6; Length 2005;
Best Local Similarity 73.7%; Pred. No. 10;
Matches 28; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Qy	3 GCTTGGGAGCTCGTCATCAACTGAGTACCC 40
Db	579 GCATTGCAGGTGATTCTTACCAACTGAGCTATCAGC 616

Search completed: January 10, 2006, 21:48:32
Job time : 329 secs

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Result No.	Score	Query Match	Length	DB ID	Description	Summaries	
1	42	100.0	4575	3	US-09-902-540-657 Sequence 657, App	RESULT 1 US-09-902-540-657	
2	32.4	77.1	258	3	US-09-540-236-104 Sequence 104, App	; Sequence 657, Application US/09902540	
3	32.4	77.1	549	3	US-09-251-99A-14551 Sequence 14851, A	; Patent No. 6833447	
4	32.4	77.1	690	3	US-09-252-99A-15110 Sequence 15110, A	; GENERAL INFORMATION:	
5	32.4	77.1	5559	2	US-08-287-442-3 Sequence 3, Appli	; APPLICANT: Goldman, Barry S.	
6	7	77.1	5559	2	US-08-459-701-3 Sequence 3, Appli	; APPLICANT: Hinkle, Gregory J.	
8	32.4	77.1	5559	2	US-08-460-298-3 Sequence 3, Appli	; APPLICANT: Slater, Roger C.	
9	32.4	77.1	5559	2	US-08-459-174-3 Sequence 3, Appli	; APPLICANT: Wiegand, Roger C.	
10	32.4	77.1	10763	2	US-08-761-258-1 Sequence 1, Appli	; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof	
11	32.4	77.1	10763	2	US-08-977-306-1 Sequence 1, Appli	; FILE REFERENCE: 38-10-15849.B	
C	13	77.1	63563	3	US-09-596-002-33 Sequence 33, Appli	; CURRENT APPLICATION NUMBER: US/09/902,540	
C	14	77.1	1830121	3	US-09-557-884-1 Sequence 1, Appli	; CURRENT FILING DATE: 2001-07-10	
C	15	77.1	1830121	3	US-09-643-90A-1 Sequence 1, Appli	; PRIORITY NUMBER: 60/217,883	
C	16	77.1	1830121	3	US-10-158-885-1 Sequence 1, Appli	; NUMBER OF SEQ ID NOS: 16825	
C	17	71.0	339	3	US-09-543-68A-3919 Sequence 3919, Ap	; SEQ ID NO: 657	
C	18	71.0	5555	3	US-09-221-01B-650 Sequence 650, App	; LENGTH: 4575	
C	19	29.8	71.0	18431	3	US-09-221-01B-1090 Sequence 1090, App	; ORGANISM: Myxococcus xanthus
C	20	29.8	71.0	640681	3	US-09-790-988-1 Sequence 1, Appli	; US-09-902-540-657
C	21	28.2	67.1	282	3	US-09-328-352-726 Sequence 726, App	; SEQ ID NO: 104
C	22	28.2	67.1	7035	3	US-09-902-540-878 Sequence 878, App	; LENGTH: 352
C	23	27.2	64.8	603	2	US-08-412-61A-85 Sequence 85, Appli	; TYPE: DNA
C	24	27.2	64.8	603	2	US-08-412-61A-86 Sequence 86, Appli	; ORGANISM: M.catarrhalis

ALIGNMENTS

RESULT 1 US-09-902-540-657						
; Sequence 657, Application US/09902540						
; Patent No. 6833447						
; GENERAL INFORMATION:						
; APPLICANT: Goldman, Barry S.						
; APPLICANT: Hinkle, Gregory J.						
; APPLICANT: Slater, Roger C.						
; APPLICANT: Wiegand, Roger C.						
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof						
; FILE REFERENCE: 38-10-15849.B						
; CURRENT APPLICATION NUMBER: US/09/902,540						
; CURRENT FILING DATE: 2001-07-10						
; PRIORITY NUMBER: 60/217,883						
; NUMBER OF SEQ ID NOS: 16825						
; SEQ ID NO: 657						
; LENGTH: 4575						
; TYPE: DNA						
; ORGANISM: Myxococcus xanthus						
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US-09-540-236-104

Query Match 77.1%; Score 32.4; DB 3; Length 258;
 Best Local Similarity 85.7%; Pred. No. 0 0019; Gaps 0;
 Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGCTTGGAAAGTCGCGTCACTGACCTACCACTGACCGC 42
 Db 113 GACCTTGCAAGTCGCGTCACTGACCTACCACTGACCGC 154

RESULT 3

US-09-252-991A-14851

; Sequence 14851, Application US/09252991A

; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252.991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 14851

; TYPE: DNA

; ORGANISM: *Pseudomonas aeruginosa*

; US-09-252-991A-14851

Query Match 77.1%; Score 32.4; DB 3; Length 549;
 Best Local Similarity 85.7%; Pred. No. 0 0022; Gaps 0;
 Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGCTTGGAAAGTCGCGTCACTGACCTACCACTGACCGC 42
 Db 478 GACCTTGCAAGTCGCGTCACTGACCTACCACTGACCGC 519

RESULT 4

US-09-252-991A-15110

; Sequence 15110, Application US/09252991A

; Patent No. 6551795

; GENENRATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252.991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 15110

; LENGTH: 690

; TYPE: DNA

; ORGANISM: *Pseudomonas aeruginosa*

; US-09-252-991A-15110

Query Match 77.1%; Score 32.4; DB 3; Length 690;
 Best Local Similarity 85.7%; Pred. No. 0 0023; Gaps 0;
 Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGCTTGGAAAGTCGCGTCACTGACCTACCACTGACCGC 42

Db 44 GACCTTGCAAGTCGCGTCACTGACCTACCACTGACCGC 85

RESULT 5

US-09-287-442-3

; Sequence 3, Application US/08287442

; Patent No. 5670350

; GENERAL INFORMATION:

; APPLICANT: Gaffney, Thomas D.

; APPLICANT: Lam, Stephen T.

; APPLICANT: Ligon, James M.

; APPLICANT: Hill, Dwight S.

; APPLICANT: Stein, Jeffrey I.

; APPLICANT: Becker, J. Ole

; TITLE OF INVENTION: Gene Activating Element

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: CIBA-BEIGY Corporation

; STREET: 7 Skyline Drive

; CITY: Hawthorne

; STATE: New York

; COUNTRY: USA

; ZIP: 10532

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/287,442

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/087,636

; FILING DATE: 01-JUL-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/908,284

; FILING DATE: 02-JUL-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/570,184

; FILING DATE: 08-AUG-1990

; ATTORNEY/AGENT INFORMATION:

; NAME: Elmer, James Scott

; REGISTRATION NUMBER: 36,129

; REFERENCE/DOCKET NUMBER: CGC 1506/CIP4

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 919-541-8614

; TELEFAX: 919-541-8689

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 5559 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULAR TYPE: DNA (Genomic)

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: *Pseudomonas fluorescens*

; STRAIN: CGA67356

; INDIVIDUAL ISOLATE: 5.6 kb EcoRI-HindIII restriction

; INDIVIDUAL ISOLATE: fragment

; IMMEDIATE SOURCE:

; CLONE: PCIB137

; FEATURE: misc_feature

; NAME/KEY: misc_feature

; LOCATION: 210..1688

; OTHER INFORMATION: /note= "ORF 1, transcribed left to

; OTHER INFORMATION: right"

; NAME/KEY: misc_feature

; LOCATION: 1906..3633

; OTHER INFORMATION: /note= "ORF 2, transcribed left to

; OTHER INFORMATION: right"

; FEATURE:

NAME/KEY: misc feature
 LOCATION: 4616..4691
 OTHER INFORMATION: /note= "glyW, transcribed right to
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 4731..5318
 OTHER INFORMATION: /note= "ORF 3, transcribed right to
 OTHER INFORMATION: left"
 US-08-287-442-3

Query Match Score 32.4; DB 2; Length 5559;
 Best Local Similarity 85.7%; Pred. No. 0.0037; 0; Mismatches 6; Indels 0; Gaps 0;
 Matches 36; Conservative 0;

Qy 1 GAGCTGGAAAGCTGTCTTACCACTGAGCTACCGGC 42
 Db 4650 GACCTGGCAGGTGCTTACCACTGAGCTACCGC 4691

RESULT 6

US-08-459-701-3

Sequence 3, Application US/08459701
 Patent No. 5686882
 GENERAL INFORMATION:
 APPLICANT: Gaffney, Thomas D.
 APPLICANT: Lam, Stephen T.
 APPLICANT: Ligon, James M.
 APPLICANT: Hill, Dwight S.
 APPLICANT: Stein, Jeffrey I.
 APPLICANT: Howell, Charles R.
 APPLICANT: Becker, J. Ole
 TITLE OF INVENTION: Gene Activating Element
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: New York
 ZIP: 10532

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459,701
 FILING DATE: 02-JUN-1995

PRIOR APPLICATION DATA:
 CLASSIFICATION: 536
 APPLICATION NUMBER: US 08/287,442
 FILING DATE: 08-AUG-1994
 APPLICATION NUMBER: US 08/087,636
 FILING DATE: 01-JUL-1993

PATENT/ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: CGC 1506/CIP4
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 919-541-8659
 INFORMATION FOR SEQ ID NO: 3:
 LENGTH: 5559 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Pseudomonas fluorescens
 STRAIN: CGA267356
 INDIVIDUAL ISOLATE: 5.6 kb EcoRI-HindIII restriction fragment
 IMMEDIATE SOURCE:
 CLONE: PCIB137

FEATURE:
 NAME/KEY: misc feature
 LOCATION: 210..1688
 OTHER INFORMATION: /note= "ORF 1, transcribed left to
 OTHER INFORMATION: right"
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1906..3633
 OTHER INFORMATION: /note= "ORF 2, transcribed left to
 OTHER INFORMATION: right"
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 4616..4691
 OTHER INFORMATION: /note= "glyW, transcribed right to
 OTHER INFORMATION: left"
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 4731..5318
 OTHER INFORMATION: /note= "ORF 3, transcribed right to
 OTHER INFORMATION: left"
 US-08-459-701-3

Query Match Score 32.4; DB 2; Length 5559;
 Best Local Similarity 85.7%; Pred. No. 0.0037; 0; Mismatches 6; Indels 0; Gaps 0;
 Matches 36; Conservative 0;

Qy 1 GAGCTGGAAAGCTGTCTTACCACTGAGCTACCGC 42
 Db 4650 GACCTGGCAGGTGCTTACCACTGAGCTACCGC 4691

RESULT 7

US-08-460-298-3

; Sequence 3, Application US/08460298
 GENERAL INFORMATION:
 Patent No. 568283
 ; Sequence 3, Application US/08460298
 ; General Information:
 APPLICANT: Gaffney, Thomas D.
 APPLICANT: Lam, Stephen T.
 APPLICANT: Ligon, James M.
 APPLICANT: Hill, Dwight S.
 APPLICANT: Stein, Jeffrey I.
 APPLICANT: Howell, Charles R.
 APPLICANT: Becker, J. Ole
 TITLE OF INVENTION: Gene Activating Element
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: New York
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459,701
 FILING DATE: 02-JUN-1995

PRIOR APPLICATION DATA:
 CLASSIFICATION: 536
 APPLICATION NUMBER: US 08/287,442
 FILING DATE: 08-AUG-1994
 APPLICATION NUMBER: US 08/087,636
 FILING DATE: 01-JUL-1993

PATENT/ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: CGC 1506/CIP4
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 919-541-8659
 INFORMATION FOR SEQ ID NO: 3:
 LENGTH: 5559 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/460,298
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/287,442
 FILING DATE: 08-AUG-1994
 APPLICATION NUMBER: US 08/087,636
 FILING DATE: 01-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/908,284
 FILING DATE: 02-JUL-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/570,184
 FILING DATE: 08-AUG-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-541-8614
 TELEFAX: 919-541-8689
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5559 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Pseudomonas fluorescens
 STRAIN: CGA267356
 INDIVIDUAL ISOLATE: 5.6 kb EcoRI-HindIII restriction
 INDIVIDUAL ISOLATE: fragment
 IMMEDIATE SOURCE:
 CLONE: PCIB137
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 210..1688
 OTHER INFORMATION: /note= "ORF 1, transcribed left to
 OTHER INFORMATION: right"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1916..3033
 OTHER INFORMATION: /note= "ORF 2, transcribed left to
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 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 4616..4691
 OTHER INFORMATION: /note= "glyW, transcribed right to
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 NAME/KEY: misc_feature
 LOCATION: 4731..5118
 OTHER INFORMATION: /note= "ORF 3, transcribed right to
 OTHER INFORMATION: left"
 US-08-460-298-3

Query Match Best Local Similarity 77.1%; Score 32.4; DB 2; Length 5559;
 Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGCTTGGAAAGCTGCGTCMACCACGTGACTAACCCGC 42
 Db 4650 GACCTGGCAAGTCGTCCTACCAACTGAGCTATCCGC 4691

RESULT 8
 US-08-459-174-3
 Sequence 3, Application US/08459174
 GENERAL INFORMATION:
 APPLICANT: Gaffney, Thomas D.
 APPLICANT: Lam, Stephen T.
 APPLICANT: Ligon, James M.
 APPLICANT: Hill, Dwight S.

APPLICANT: Stein, Jeffrey I.
 APPLICANT: Howell, Charles R.
 APPLICANT: Becker, J. Ole R.
 TITLE OF INVENTION: Gene Activating Element
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: New York
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentnet Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459,174
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/287,442
 FILING DATE: 08-AUG-1994
 APPLICATION NUMBER: US 08/087,636
 FILING DATE: 01-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/908,284
 FILING DATE: 02-JUL-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/570,184
 FILING DATE: 08-AUG-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: CGC 1506/CIP4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-541-8614
 TELEFAX: 919-541-8689
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5559 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Pseudomonas fluorescens
 STRAIN: CGA267356
 INDIVIDUAL ISOLATE: 5.6 kb EcoRI-HindIII restriction
 INDIVIDUAL ISOLATE: fragment
 IMMEDIATE SOURCE:
 CLONE: PCIB137
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 210..1688
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 OTHER INFORMATION: right"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1916..3033
 OTHER INFORMATION: /note= "ORF 2, transcribed left to
 OTHER INFORMATION: right"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 4616..4691
 OTHER INFORMATION: /note= "glyW, transcribed right to
 OTHER INFORMATION: left"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 4731..5118
 OTHER INFORMATION: /note= "ORF 3, transcribed right to
 OTHER INFORMATION: left"
 US-08-460-298-3

Query Match Best Local Similarity 77.1%; Score 32.4; DB 2; Length 5559;
 Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GGCTTGGAAAGCTGCGTCMACCACGTGACTAACCCGC 42
 Db 4650 GACCTGGCAAGTCGTCCTACCAACTGAGCTATCCGC 4691

RESULT 8
 US-08-459-174-3
 Sequence 3, Application US/08459174
 GENERAL INFORMATION:
 APPLICANT: Gaffney, Thomas D.
 APPLICANT: Lam, Stephen T.
 APPLICANT: Ligon, James M.
 APPLICANT: Hill, Dwight S.

APPLICANT: Stein, Jeffrey I.
 APPLICANT: Howell, Charles R.
 APPLICANT: Becker, J. Ole R.
 TITLE OF INVENTION: Gene Activating Element
 NUMBER OF SEQUENCES: 9
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: New York
 COUNTRY: USA
 ZIP: 10532
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentnet Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/459,174
 FILING DATE: 02-JUN-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/287,442
 FILING DATE: 08-AUG-1994
 APPLICATION NUMBER: US 08/087,636
 FILING DATE: 01-JUL-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/908,284
 FILING DATE: 02-JUL-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/570,184
 FILING DATE: 08-AUG-1990
 ATTORNEY/AGENT INFORMATION:
 NAME: Elmer, James Scott
 REGISTRATION NUMBER: 36,129
 REFERENCE/DOCKET NUMBER: CGC 1506/CIP4
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 919-541-8614
 TELEFAX: 919-541-8689
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5559 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Pseudomonas fluorescens
 STRAIN: CGA267356
 INDIVIDUAL ISOLATE: 5.6 kb EcoRI-HindIII restriction
 INDIVIDUAL ISOLATE: fragment
 IMMEDIATE SOURCE:
 CLONE: PCIB137
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 210..1688
 OTHER INFORMATION: /note= "ORF 1, transcribed left to
 OTHER INFORMATION: right"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1916..3033
 OTHER INFORMATION: /note= "ORF 2, transcribed left to
 OTHER INFORMATION: right"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 4616..4691
 OTHER INFORMATION: /note= "glyW, transcribed right to
 OTHER INFORMATION: left"
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 4731..5118
 OTHER INFORMATION: /note= "ORF 3, transcribed right to
 OTHER INFORMATION: left"
 US-08-460-298-3

OTHER INFORMATION: /note= "ORF 3, transcribed right to left"
 US-08-459-174-3

Query Match 77.1%; Score 32.4; DB 2; Length 5559;
 Best Local Similarity 85.7%; Pred. No. 0.0037; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GACCTGGAAAGTCGTCTTACCAACTGAGTACCCACCGC 42
 Db 4650 GACCTGGAAAGTCGTCTTACCAACTGAGTACCCACCGC 4691

RESULT 9
 PCT-US93-06300A-3

Sequence 3, Application PC/TU9306300A

GENERAL INFORMATION:
 APPLICANT: CIBA-GEIGY AG
 APPLICANT: Klybeckstrasse 141
 APPLICANT: 4002 Basle
 APPLICANT: Switzerland
 APPLICANT: 125 Tradescant Road
 APPLICANT: Chapel Hill, NC 27514
 APPLICANT: USA
 APPLICANT: 8900 Jeannew Court
 APPLICANT: Raleigh, NC 27613
 APPLICANT: USA
 APPLICANT: 27278
 APPLICANT: Hill, Dwight Steven
 APPLICANT: 311 Melanie Lane
 APPLICANT: Cary, NC 27511
 APPLICANT: USA
 APPLICANT: Stein, Jeffrey I.
 APPLICANT: 3725 Surry Trail
 APPLICANT: Hillsborough, NC 27278
 APPLICANT: USA
 APPLICANT: Howall, Charles R.
 APPLICANT: 805 Avondale
 APPLICANT: Bryan, TX 77802
 APPLICANT: USA
 APPLICANT: Becker, J. Ole
 APPLICANT: 6164 Osevego
 APPLICANT: Riverside, CA 92506
 APPLICANT: USA
 APPLICANT: Ligon, James M.
 APPLICANT: 120 Marquette Drive
 APPLICANT: Cary, NC 27513
 APPLICANT: USA

TITLE OF INVENTION: Gene Activating Element
 NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:
 ADDRESSEE: CIBA-GEIGY Corporation
 STREET: 7 Skyline Drive
 CITY: Hawthorne
 STATE: New York
 COUNTRY: USA
 ZIP: 10532

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/06300A
 FILING DATE: 02-JUL-1993
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/908,284
 FILING DATE: 02-JUL-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: SPURLI, W. Murray
 REGISTRATION NUMBER: 32,943
 REFERENCE/DOCKET NUMBER: S-18210/A/CGC1506/PC

TELECOMMUNICATION INFORMATION:

TELEPHONE: (919)541-8615
 TELEFAX: (919)541-8689
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5559 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: *Pseudomonas fluorescens*
 STRAIN: CGA267356
 INDIVIDUAL ISOLATE: 5.6 kb EcoRI-HindIII restriction
 IMMEDIATE SOURCE:
 CLONE: PCIB137

FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 210..1668
 OTHER INFORMATION: /note= "ORF 1, transcribed left to right"
 FEATURES:
 NAME/KEY: misc_feature
 LOCATION: 1906..3633
 OTHER INFORMATION: /note= "ORF 2, transcribed left to right"
 FEATURES:
 NAME/KEY: misc_feature
 LOCATION: 4616..4691
 OTHER INFORMATION: /note= "glyW, transcribed right to left"
 FEATURES:
 NAME/KEY: misc_feature
 LOCATION: 4731..5318
 OTHER INFORMATION: /note= "ORF 3, transcribed right to left"
 PCT-US93-06300A-3

Query Match 77.1%; Score 32.4; DB 6; Length 5559;
 Best Local Similarity 85.7%; Pred. No. 0.0037; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGCTTGGAAAGCTCTAACCAACTGAGTACCCACCGC 42
 Db 4650 GACCTGGAAAGTCGTCTTACCAACTGAGTACCCACCGC 4691

RESULT 10
 US-08-761-258-1

Sequence 1, Application US/08761258
 Patent No. 5756087

GENERAL INFORMATION:
 APPLICANT: Ligon, James M.
 APPLICANT: Hill, Dwight S.
 APPLICANT: Lam, Stephen T.
 APPLICANT: Gaffney, Thomas D.
 APPLICANT: Torkewitz, Nancy
 TITLE OF INVENTION: Genetically Modified *Pseudomonas* Strains
 TITLE OF INVENTION: with Enhanced Biocontrol Activity
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ciba-Geigy Corporation
 STREET: 520 White Plains Road, P.O. Box 2005
 CITY: Tarrytown
 STATE: NY
 COUNTRY: USA
 ZIP: 10591

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US93/06300A
 FILING DATE: 02-JUL-1993
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/908,284
 FILING DATE: 02-JUL-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: SPURLI, W. Murray
 REGISTRATION NUMBER: 32,943
 REFERENCE/DOCKET NUMBER: S-18210/A/CGC1506/PC

TELECOMMUNICATION INFORMATION:

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/761,258
 FILING DATE: 4/24
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919) 541-8387
 TELEFAX: (919) 541-8689
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10763 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Pseudomonas fluorescens
 STRAIN: CGA267356 (aka MOCG134 and aka BL915)
 IMMEDIATE SOURCE:
 CLONE: Plasmid pE11

FEATURE:
 NAME/KEY: misc feature
 LOCATION: 210..1688 /product= "methyltransferase"
 OTHER INFORMATION: /note= "Coding sequence for methyltransferase has homology to the cheR and frzF genes from E. coli and Myxococcus xanthus,
 OTHER INFORMATION: the cheR and frzF genes from E. coli and Myxococcus xanthus,
 OTHER INFORMATION: respectively."
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1906..333 /product= "sensor kinase"
 OTHER INFORMATION: /note= "Coding sequence for sensor kinase has homology to the
 OTHER INFORMATION: rcsc, frzB, and bvgS genes of E. coli, M. xanthus, and
 OTHER INFORMATION: Bordetella pertussis, respectively."
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: complement (4616..4691) /product= "tRNA"
 OTHER INFORMATION: /note= "complementary DNA strand) Homology to glyW from E.
 OTHER INFORMATION: Bordetella pertussis, respectively."
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: complement (4731..5318) /product= "tRNA"
 OTHER INFORMATION: /note= "Cdp-diacylglycerol-3-phosphate-3-phosphatidyltrans."
 OTHER INFORMATION: /note= "Coding sequence for
 OTHER INFORMATION: CDP-diacylglycerol-glycerol-3-phosphate-3-phosphatidyltrans."
 OTHER INFORMATION: /note= "Coding sequence for
 OTHER INFORMATION: CDP-diacylglycerol-glycerol-3-phosphate-3-phosphatidyltrans."
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: complement (5574..7397) /product= "UVR exonuclease subunit C"
 OTHER INFORMATION: /note= "Coding sequence for UVR exonuclease subunit C has homology to uvrC."
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: complement (7400..8041) /function= "response"
 OTHER INFORMATION: /note= "regulator/transcription activator"
 OTHER INFORMATION: /product= "gaca (aka gafA)"
 OTHER INFORMATION: /note= "Coding sequence for gacA (aka gafA) has homology to
 OTHER INFORMATION: uvr and gacA genes of E. coli and Ps. fluorescens,
 OTHER INFORMATION: respectively."
 US-08-761-258-1

Query Match 77.1%; Score 32.4%; DB 2; Length 10763;

Best Local Similarity 85.7%; Pred. No. 0.0043; Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

RESUNIT 11
 US-08-977-306-1
 Sequence 1, Application US/08977306
 / Patent No. 5955348
 / GENERAL INFORMATION:
 / APPLICANT: Ligon, James M.
 / APPLICANT: Gaffney, Thomas D.
 / APPLICANT: Hill, Dwight S.
 / APPLICANT: Torkewitz, Nancy M.
 / TITLE OF INVENTION: Genetically Modified Pseudomonas Strains
 / TITLE OF INVENTION: with Enhanced Biocatalyst Activity
 / NUMBER OF SEQUENCES: 11
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: No. 5955348 Bartis Corporation
 / STREET: 3054 Cornwallis Road
 / CITY: Research Triangle Park
 / STATE: NC
 / COUNTRY: USA
 / ZIP: 27709
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/977,306
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Meigs, J. Timothy
 REGISTRATION NUMBER: 38,241
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (919) 541-8587
 TELEFAX: (919) 541-8689
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10763 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Pseudomonas fluorescens
 STRAIN: CGA267356 (aka MOCG134 and aka BL915)
 IMMEDIATE SOURCE:
 CLONE: Plasmid pE11
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 210..1688
 OTHER INFORMATION: /product= "methyltransferase"
 OTHER INFORMATION: /note= "Coding sequence for methyltransferase has homology to the cheR and frzF genes from E. coli and Myxococcus xanthus,
 OTHER INFORMATION: the cheR and frzF genes from E. coli and Myxococcus xanthus,
 OTHER INFORMATION: respectively."
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: 1906..333
 OTHER INFORMATION: /product= "sensor kinase"
 OTHER INFORMATION: /note= "Coding sequence for sensor kinase has homology to the
 OTHER INFORMATION: rcsc, frzB, and bvgS genes of E. coli, M. xanthus, and
 OTHER INFORMATION: Bordetella pertussis, respectively."
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: complement (4616..4691)
 OTHER INFORMATION: /product= "tRNA"
 OTHER INFORMATION: /note= "complementary DNA strand) Homology to glyW from E.
 OTHER INFORMATION: Bordetella pertussis, respectively."
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: complement (4731..5318)
 OTHER INFORMATION: /product= "tRNA"
 OTHER INFORMATION: /note= "Cdp-diacylglycerol-3-phosphate-3-phosphatidyltrans."
 OTHER INFORMATION: /note= "Coding sequence for
 OTHER INFORMATION: CDP-diacylglycerol-glycerol-3-phosphate-3-phosphatidyltrans."
 OTHER INFORMATION: /note= "Coding sequence for
 OTHER INFORMATION: CDP-diacylglycerol-glycerol-3-phosphate-3-phosphatidyltrans."
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: complement (5574..7397)
 OTHER INFORMATION: /product= "UVR exonuclease subunit C"
 OTHER INFORMATION: /note= "Coding sequence for UVR exonuclease subunit C has homology to uvrC."
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 NAME/KEY: misc feature
 LOCATION: 7400..8041
 OTHER INFORMATION: /function= "response"
 OTHER INFORMATION: /note= "regulator/transcription activator"
 OTHER INFORMATION: /product= "gaca (aka gafA)"
 OTHER INFORMATION: /note= "Coding sequence for gacA (aka gafA) has homology to
 OTHER INFORMATION: uvr and gacA genes of E. coli and Ps. fluorescens,
 OTHER INFORMATION: respectively."
 US-08-761-258-1

Query Match 77.1%; Score 32.4%; DB 2; Length 10763;

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; LOCATION: complement (4616..4591)
; OTHER INFORMATION: /product= "tRNA"
; OTHER INFORMATION: /note= "(complementary DNA strand) Homology to glyW from E.
; OTHER INFORMATION: coli."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: complement (4711..5518)
; OTHER INFORMATION: /product=
; OTHER INFORMATION: "CDP-diacylglycerol-3-phosphate-3-phosphatidyltransf
; OTHER INFORMATION: atidytran."
; OTHER INFORMATION: /note= "Coding sequence for
; OTHER INFORMATION: CDP-diacylglycerol-3-phosphate-3-phosphatidyltransf
; OTHER INFORMATION: se has homology to pgSA."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: complement (5574..7397)
; OTHER INFORMATION: /product= "UVR exonuclease subunit
; OTHER INFORMATION: C"
; OTHER INFORMATION: /note= "Coding sequence for UVR exonuclease subunit C has
; OTHER INFORMATION: homology to uvrc."
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: complement (7400..8041)
; OTHER INFORMATION: /function= "response
; OTHER INFORMATION: regulator/transcription activator"
; OTHER INFORMATION: /product= "gaca (aka gafA)"
; OTHER INFORMATION: /note= "Coding sequence for gaca (aka gafA) has homology to
; OTHER INFORMATION: uvr and gaca genes of E. coli and Ps. fluorescens,
; OTHER INFORMATION: respectively."
US-08-9177-306-1

Query Match      77.1% Score 32.4; DB 2; Length 10763;
Best Local Similarity 85.7%; Pred. No. 0.0043; Mismatches 6; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy          1 GAGTTGGAAAGCTGCTACGAACTGAGTACCCCGC 42
Db          4650 GACCTTGGCAAGCTGTGTCCTACCAACTGAGCTATCCGC 4691

RESULT 12
US-09-556-002-25/c
Sequence 25, Application US/09596002
Patent No. 6632636
GENERAL INFORMATION:
APPLICANT: Lagace, Robert, E.
APPLICANT: Patterson, Chandra
APPLICANT: Berg, Kim, L.
TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELIA CATARRHALIS GENOME
FILE REFERENCE: PM-0008-4 US
CURRENT APPLICATION NUMBER: US/09/596,002
CURRENT FILING DATE: 2000-06-16
PRIOR APPLICATION NUMBER: 60/140,121
PRIOR FILING DATE: 1999-06-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PERL Program
SEQ ID NO 25
LENGTH: 31147
TYPE: DNA
ORGANISM: M. catarrhalis
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte template ID No. 6632636 25
PUBLICATION INFORMATION:
US-09-556-002-25

Query Match      77.1% Score 32.4; DB 3; Length 31147;
Best Local Similarity 85.7%; Pred. No. 0.0054; Mismatches 6; Indels 0; Gaps 0;
Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy          1 GAGTTGGAAAGCTGCTACGAACTGAGCTACCCCGC 42
Db          13927 GACCTTGGCAAGCTGTGTCCTACCAACTGAGCTATCCGC 13886

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RESULT 13
 US-09-596-002-33/C
 ; Sequence 33, Application US/09596002
 ; Patent No. 6632636
 ; GENERAL INFORMATION:
 ; APPLICANT: Patterson, Chandra
 ; APPLICANT: Berg, Kim, L.
 ; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
 ; FILE REFERENCE: PM-0008-4 US
 ; CURRENT APPLICATION NUMBER: US/09/596,002
 ; CURRENT FILING DATE: 2000-06-16
 ; PRIOR APPLICATION NUMBER: 60/140,121
 ; PRIOR FILING DATE: 1999-06-18
 ; NUMBER OF SEQ ID NOS: 41
 ; SOFTWARE: PERL program
 ; SEQ ID NO 33
 ; LENGTH: 63563
 ; TYPE: DNA
 ; ORGANISM: M. catarrhalis
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte template ID No. 6612636 33
 ; PUBLIC "-//IUB/IUPAC//PUBMLT//EN//IDN//> INFORMATION:
 ; US-09-596-002-33

	Query Match	Score 32.4;	DB 3;	Length 63563;
Qy	Best Local Similarity Matches 36; Conservative 36;	Pred. No. 0. 0.0044; 0; Mismatches 0;	Indels 6;	Gaps 0;
Db	1 GAGCTTGGAAGCTCTGCTCTACCAACTSAGCTAACCCG 1051 GACCTTGCAAGGTCTACCAACTSAGCTATTCCCGC 1010			

RESULT 14
 US-09-557-884-1/C
 ; Sequence 1, Application US/09557884
 ; Patent No. 650581
 ; GENERAL INFORMATION:
 ; APPLICANT: Fleischmann et al.
 ; TITLE OF INVENTION: The Haemophilus influenzae Rd Genome, Fragments
 ; NUMBER OF SEQUENCES: 1
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEES: Human Genome Sciences, Inc.
 ; STREET: 9410 Key West Avenue
 ; CITY: Rockville
 ; STATE: MD
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3 1/2 inch diskette
 ; COMPUTER: Dell Pentium
 ; OPERATING SYSTEM: MS DOS v6.22
 ; SOFTWARE: ASCII Text
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/557,884
 ; FILING DATE: 25-Apr-2000
 ; CLASSIFICATION: <Unknown>
 ; PRIORITY APPLICATION DATA:
 ; APPLICATION NUMBER: 08/476,102
 ; FILING DATE: JUN-5-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Michelle S Marks
 ; REGISTRATION NUMBER: 41,971
 ; REFERENCE/DOCKET NUMBER: PB186P3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 301-309-8439
 ; TELEFAX: 301-309-8504

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1830121 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-557-884-1

Query Match Best Local Similarity Score DB Length
 Matches 36; Conservative 85.7%; Pred. No. 0.014; 3; 1830121;
 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGCTTGGAAACTCGTCCTACCAACTGAGCTTACCAACGC 42
 Db 90995 GACCTTGGCAAGTCGTGCTTACAACTGAGCTATTCCGGC 90954

Search completed: January 10, 2006, 19:28:15
 Job time : 150 secs

RESULT 15
 US-09-643-990A-1/c
 Sequence 1, Application US/09643990A
 Patent No. 658289

GENERAL INFORMATION:
 APPLICANT: Robert D. Fleischmann
 Mark D. Adams
 Owen White
 Hamilton O. Smith
 Craig Venter
 Owen White

J. Craig Venter
 Hamilton O. Smith
 Owen White

TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville,
 STATE: MD
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3 1/2 inch diskette
 COMPUTER: Dell Pentium
 OPERATING SYSTEM: MS DOS v6.22
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/643,990A
 FILING DATE: 23-Aug-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/487,429
 FILING DATE: 1995-06-07
 APPLICATION NUMBER: 08/426,787
 FILING DATE: 1995-04-21
 ATTORNEY/AGENT INFORMATION:
 NAME: Kenley K. Hoover
 REGISTRATION NUMBER: 40,302
 REFERENCE/DOCKET NUMBER: PP186P1C1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-610-5790
 TELEFAX: 310-309-8439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
 LENGTH: 1830121 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 1:
 US-09-643-990A-1

Query Match Best Local Similarity Score DB Length
 Matches 36; Conservative 85.7%; Pred. No. 0.014; 3; 1830121;
 0; Mismatches 6; Indels 0; Gaps 0;

GenCore version 5.1.6
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OM nucleic - nucleic search, using bw model

Run on: January 10, 2006, 18:22:31 ; Search time 815 Seconds
 (without alignments)
 426.152 Million cell updates/sec

Title: US-10-645-818-5

Perfect score: 42

Sequence: 1 gagcttggaaaggctcggtc.....accaacttaggctaccaccgc 42

Scoring table: IDENTITY_NUC Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

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Database : Published Applications_NA_Main:*
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  2: /cgn2_6/_ptodata1/pupbna/US08_PUBCOMB.seq:*
  3: /cgn2_6/_ptodata1/pupbna/US09A_PUBCOMB.seq:*
  4: /cgn2_6/_ptodata1/pupbna/US10A_PUBCOMB.seq:*
  5: /cgn2_6/_ptodata1/pupbna/US10C_PUBCOMB.seq:*
  6: /cgn2_6/_ptodata1/pupbna/US10C_PUBCOMB.seq:*
  7: /cgn2_6/_ptodata1/pupbna/US10D_PUBCOMB.seq:*
  8: /cgn2_6/_ptodata1/pupbna/US10E_PUBCOMB.seq:*
  9: /cgn2_6/_ptodata1/pupbna/US10E_PUBCOMB.seq:*
  10: /cgn2_6/_ptodata1/pupbna/US11_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

ALIGNMENTS

Sequence 1068, AP

Sequence 1, Appli

Sequence 85, App

Sequence 86, Appli

Sequence 85, Appli

Sequence 86, Appli

Sequence 89, Appli

Sequence 8, Appli

Sequence 8, Appli

Sequence 1068, AP

Sequence 1, Appli

Sequence 1, Appli

Sequence 1, Appli

Sequence 4, Appli

Sequence 4, Appli

Sequence 322, App

Sequence 131, App

Sequence 132, App

Sequence 131, App

Sequence 132, App

Sequence 154, App

PRIOR FILING DATE: 2002-08-21
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 12
 LENGTH: 74
 TYPE: DNA
 ORGANISM: Myxococcus xanthus
 US-10-645-818-12

Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
 US-10-645-818-7
 Sequence 7, Application US/10645818
 Publication No. US20040447620A1
 GENERAL INFORMATION:
 APPLICANT: Kosan Biosciences, Inc.
 APPLICANT: Julian, Bryan
 TITLE OF INVENTION: TRANSFORMATION SYSTEM BASED ON THE INTEGRASE GENE AND ATTACHMENT SITE FOR MYXOCOCCUS XANTHUS
 TITLE OF INVENTION: BACTERIOPHAGE MX9
 FILE REFERENCE: 300622009940
 CURRENT APPLICATION NUMBER: US 60/405,196
 PRIOR FILING DATE: 2003-08-21
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 7
 LENGTH: 257
 TYPE: DNA
 ORGANISM: Bacteriophage MX9
 US-10-645-818-7

Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
 US-10-645-818-3
 Sequence 3, Application US/10645818
 Publication No. US20040447620A1
 GENERAL INFORMATION:
 APPLICANT: Kosan Biosciences, Inc.
 APPLICANT: Julian, Bryan
 TITLE OF INVENTION: TRANSFORMATION SYSTEM BASED ON THE INTEGRASE GENE AND ATTACHMENT SITE FOR MYXOCOCCUS XANTHUS
 TITLE OF INVENTION: BACTERIOPHAGE MX9
 FILE REFERENCE: 300622009940
 CURRENT APPLICATION NUMBER: US 60/405,196
 PRIOR FILING DATE: 2003-08-21
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 360
 TYPE: DNA
 ORGANISM: Bacteriophage MX9
 US-10-645-818-3

Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 US-10-645-818-4
 Sequence 4, Application US/10645818
 Publication No. US20040247620A1
 GENERAL INFORMATION:
 APPLICANT: Kosan Biosciences, Inc.
 APPLICANT: Julian, Bryan
 TITLE OF INVENTION: TRANSFORMATION SYSTEM BASED ON THE INTEGRASE GENE AND ATTACHMENT SITE FOR MYXOCOCCUS XANTHUS
 TITLE OF INVENTION: BACTERIOPHAGE MX9
 FILE REFERENCE: 300622009940
 CURRENT FILING DATE: 2003-08-20
 PRIOR APPLICATION NUMBER: US 60/405,196
 PRIOR FILING DATE: 2002-08-21
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 4
 LENGTH: 360
 TYPE: DNA
 ORGANISM: Bacteriophage MX9
 US-10-645-818-4

Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 6
 US-10-645-818-1
 Sequence 1, Application US/10645818
 Publication No. US20040247620A1
 GENERAL INFORMATION:
 APPLICANT: Kosan Biosciences, Inc.
 APPLICANT: Julian, Bryan
 TITLE OF INVENTION: TRANSFORMATION SYSTEM BASED ON THE INTEGRASE GENE AND ATTACHMENT SITE FOR MYXOCOCCUS XANTHUS
 TITLE OF INVENTION: BACTERIOPHAGE MX9
 FILE REFERENCE: 300622009940
 CURRENT APPLICATION NUMBER: US 10/645,818
 CURRENT FILING DATE: 2003-08-20
 PRIOR APPLICATION NUMBER: US 60/405,196
 PRIOR FILING DATE: 2002-08-21
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 1
 LENGTH: 1647
 TYPE: DNA
 ORGANISM: Bacteriophage MX9
 US-10-645-818-1

Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 7
 US-10-645-818-2
 Sequence 2, Application US/10645818
 Publication No. US20040247620A1
 GENERAL INFORMATION:
 APPLICANT: Kosan Biosciences, Inc.
 APPLICANT: Julian, Bryan
 TITLE OF INVENTION: TRANSFORMATION SYSTEM BASED ON THE INTEGRASE GENE AND ATTACHMENT SITE FOR MYXOCOCCUS XANTHUS
 TITLE OF INVENTION: BACTERIOPHAGE MX9
 FILE REFERENCE: 300622009940
 CURRENT APPLICATION NUMBER: US 60/405,196
 PRIOR APPLICATION NUMBER: US 60/405,196
 PRIOR FILING DATE: 2003-08-21
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 360
 TYPE: DNA
 ORGANISM: Bacteriophage MX9
 US-10-645-818-2

Query Match Score 100.0%; Best Local Similarity 100.0%; Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 8
 US-10-645-818-3
 Sequence 3, Application US/10645818
 Publication No. US20040247620A1
 GENERAL INFORMATION:
 APPLICANT: Kosan Biosciences, Inc.
 APPLICANT: Julian, Bryan
 TITLE OF INVENTION: TRANSFORMATION SYSTEM BASED ON THE INTEGRASE GENE AND ATTACHMENT SITE FOR MYXOCOCCUS XANTHUS
 TITLE OF INVENTION: BACTERIOPHAGE MX9
 FILE REFERENCE: 300622009940
 CURRENT APPLICATION NUMBER: US 60/405,196
 PRIOR APPLICATION NUMBER: US 60/405,196
 PRIOR FILING DATE: 2003-08-21
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 360
 TYPE: DNA
 ORGANISM: Bacteriophage MX9
 US-10-645-818-3

RESULT 7
 US-09-815-242-3781/c
 ; Sequence 3781, Application US/09815242
 ; GENERAL INFORMATION:
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes
 ; FILE REFERENCE: ELTRIA_011A
 ; CURRENT APPLICATION NUMBER: US/09/815,242
 ; CURRENT FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; NUMBER OF SEQ ID NOS: 14110
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 3781
 ; LENGTH: 557
 ; TYPE: DNA
 ; ORGANISM: *Salmonella typhimurium*
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(657)
 ; OTHER INFORMATION: n = A,T,C or G
 ; us-09-815-242-3781

Query Match 77.1%; Score 32.4; DB 3; Length 657;
 Best Local Similarity 85.7%; Pred. No. 0 004; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGCTTGGAACTCGRGTCTACCAACTGAGCTACCCGC 42
 Db 579 GACCTTGGAACTCGRGTCTACCAACTGAGCTACCCGC 538

RESULT 8
 US-10-795-159-201
 ; Sequence 201, Application US/10795159
 ; Publication No. US2005021439A1

; GENERAL INFORMATION:
 ; APPLICANT: BAKALETZ et al.
 ; TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPABLE H. INFLUENZAE
 ; FILE REFERENCE: 28335/38815A
 ; CURRENT APPLICATION NUMBER: US/10/795,159
 ; CURRENT FILING DATE: 2004-03-05
 ; PRIOR APPLICATION NUMBER: US 60/453,134
 ; NUMBER OF SEQ ID NOS: 771
 ; SEQ ID NO: 201
 ; LENGTH: 1960
 ; TYPE: DNA
 ; ORGANISM: H. influenzae
 ; us-10-795-159-201

Query Match 77.1%; Score 32.4; DB 9; Length 1960;
 Best Local Similarity 85.7%; Pred. No. 0 0046; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGCTTGGAACTCGRGTCTACCAACTGAGCTACCCGC 42
 Db 760 GACCTTGGAACTCGRGTCTACCAACTGAGCTACCCGC 801

RESULT 9
 US-10-795-159-492/c
 ; Sequence 492, Application US/10795159
 ; Publication No. US2005021439A1

; GENERAL INFORMATION:
 ; APPLICANT: BAKALETZ et al.
 ; TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPABLE H. INFLUENZAE
 ; FILE REFERENCE: 28335/38815A
 ; CURRENT APPLICATION NUMBER: US/10/795,159
 ; CURRENT FILING DATE: 2004-03-05
 ; PRIOR APPLICATION NUMBER: US 60/453,134
 ; NUMBER OF SEQ ID NOS: 771
 ; SEQ ID NO: 492
 ; LENGTH: 5436
 ; TYPE: DNA
 ; ORGANISM: H. influenzae
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (101)..(101)
 ; OTHER INFORMATION: n = a, c, g, or t
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (5156)..(5156)
 ; OTHER INFORMATION: (5156)..(5156)
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (5265)..(5265)
 ; OTHER INFORMATION: (5265)..(5265)
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (5294)..(5294)
 ; OTHER INFORMATION: n = a, c, g, or t
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (5391)..(5392)
 ; OTHER INFORMATION: (5391)..(5392)

Query Match 77.1%; Score 32.4; DB 9; Length 5436;
 Best Local Similarity 85.7%; Pred. No. 0 0052; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGCTTGGAACTCGRGTCTACCAACTGAGCTACCCGC 42
 Db 5153 GACCTTGGAACTCGRGTCTACCAACTGAGCTACCCGC 5112

RESULT 10
 US-10-795-159-575/c
 ; Sequence 575, Application US/10795159
 ; Publication No. US2005021439A1

; GENERAL INFORMATION:
 ; APPLICANT: BAKALETZ et al.
 ; TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPABLE H. INFLUENZAE
 ; FILE REFERENCE: 28335/38815A
 ; CURRENT APPLICATION NUMBER: US/10/795,159
 ; CURRENT FILING DATE: 2004-03-05
 ; PRIOR APPLICATION NUMBER: US 60/453,134
 ; NUMBER OF SEQ ID NOS: 771
 ; SEQ ID NO: 575
 ; LENGTH: 1960
 ; TYPE: DNA
 ; ORGANISM: H. influenzae
 ; us-10-795-159-575

```

; LENGTH: 28871
; ORGANISM: H. influenzae
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (82)-(82)
; OTHER INFORMATION: n = a, c, g, or t
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (5660)..(5660)
; OTHER INFORMATION: n = a, c, g, or t
; FEATURE: misc_feature
; NAME/KEY: misc_feature
; LOCATION: (28833)..(28833)
; OTHER INFORMATION: n = a, c, g, or t
; SEQ ID NO: 33
; LENGTH: 63563
; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
; US-10-672-787-33

Query Match          77.1%; Score 32.4; DB 7; Length 63563;
Best Local Similarity 85.7%; Pred. No. 0.0072;
Matches 36; Conservative 6; Indels 0; Gaps 0;

Qy    1 GAGCTTGGAAAGCTCGTCCTACCAACTGAGCTTACCCGC 42
Db    1051 GACCTTGGCAAGGTCTGTCTACCAACTGAGCTTACCCGC 1010

RESULT 13
US-10-795-159-684/c
; Sequence 684, Application US/10795159
; Publication No. US20050221439A1
; GENERAL INFORMATION:
; APPLICANT: BAKALETZ, et al.
; TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPEABLE H. INFLUENZAE
; FILE REFERENCE: 283335/38815A
; CURRENT APPLICATION NUMBER: US/10/795,159
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 60/453,134
; PRIOR FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 771
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 684
; LENGTH: 411576

TYPE: DNA
ORGANISM: H. influenzae
FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: (93601)..(93603)
OTHER INFORMATION: n is a, c, g, or t
FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: (93620)..(93620)
OTHER INFORMATION: n is a, c, g, or t
FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: (93622)..(93625)
OTHER INFORMATION: n is a, c, g, or t
FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: (138551)..(138581)
OTHER INFORMATION: n is a, c, g, or t
US-10-795-159-684

Query Match          77.1%; Score 32.4; DB 9; Length 411576;
Best Local Similarity 85.7%; Pred. No. 0.0091;
Matches 36; Conservative 6; Indels 0; Gaps 0;

Qy    1 GAGCTTGGAAAGCTCGTCCTACCAACTGAGCTTACCCGC 42
Db    76404 GACCTTGGCAAGGTCTGTCTACCAACTGAGCTTACCCGC 76363

RESULT 14
US-10-795-159-685/c
; Sequence 685, Application US/10795159
; Publication No. US20050221439A1
; GENERAL INFORMATION:
; APPLICANT: BAKALETZ, et al.
; TITLE OF INVENTION: GENES OF AN OTITIS MEDIA ISOLATE OF NONTYPEABLE H. INFLUENZAE
; FILE REFERENCE: 283335/38815A
; CURRENT APPLICATION NUMBER: US/10/795,159
; CURRENT FILING DATE: 2004-03-05
; PRIOR APPLICATION NUMBER: US 60/453,134
; PRIOR FILING DATE: 2003-03-06
; NUMBER OF SEQ ID NOS: 771

Query Match          77.1%; Score 32.4; DB 7; Length 31147;
Best Local Similarity 85.7%; Pred. No. 0.0065;
Matches 36; Conservative 6; Indels 0; Gaps 0;

Qy    1 GAGCTTGGAAAGCTCGTCCTACCAACTGAGCTTACCCGC 42
Db    13927 GACCTTGGCAAGGTCTGTCTACCAACTGAGCTTACCCGC 13886

RESULT 12
US-10-672-787-33/c
; Sequence 33, Application US/10672287
; Publication No. US200406755A1
; GENERAL INFORMATION:
; APPLICANT: PATTERSON, Chandra
; APPLICANT: BERG, Kim, L.
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCES OF MORAXELLA CATARRHALIS GENOME
; FILE REFERENCE: ELITRA_025C1
; CURRENT APPLICATION NUMBER: US/10/672,787
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 09/596,002
; PRIOR FILING DATE: 2000-06-16
; SOFTWARE: PERL Program
; SEQ ID NO: 25
; LENGTH: 31147
; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
; SEQ ID NO: 33
; LENGTH: 63563
; TYPE: DNA
; ORGANISM: Moraxella catarrhalis
; US-10-672-787-33

Query Match          77.1%; Score 32.4; DB 7; Length 31147;
Best Local Similarity 85.7%; Pred. No. 0.0065;
Matches 36; Conservative 6; Indels 0; Gaps 0;

Qy    1 GAGCTTGGAAAGCTCGTCCTACCAACTGAGCTTACCCGC 42
Db    13927 GACCTTGGCAAGGTCTGTCTACCAACTGAGCTTACCCGC 13886

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SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 685
 LENGTH: 908766
 TYPE: DNA
 ORGANISM: H. influenzae
 FEATURE: misc feature
 LOCATION: (9223)..(9223)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (33640)..(33640)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (22404)..(22404)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (22495)..(22495)
 OTHER INFORMATION: n is a, c, g, or t
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (908641)..(908641)
 OTHER INFORMATION: n is a, c, g, or t
 US-10-795-159-685

Query Match Similarity 77.1%; Score 32.4%; DB 9; Length 908766;
 Best Local Similarity 85.7%; Pped. No 0; 01; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGCTTGGAAACTCGTCCTACCAACTGAGCTTACACCGC 42
 Db 748266 GACCTTGGAAACTCGTCCTACCAACTGAGCTTACCGC 748225

RESULT 15
 US-10-329-670-1/c
 Sequence 1, Application US/10329670
 Publication No. US2004018503A1
 GENERAL INFORMATION:
 APPLICANT: Fleischmann et al.
 TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, Frag
 FILE REFERENCE: PB186P1
 CURRENT APPLICATION NUMBER: US/10/329_670
 CURRENT FILING DATE: 2002-12-24
 PRIOR APPLICATION NUMBER: US 09/643,990
 PRIOR FILING DATE: 2000-08-23
 PRIOR APPLICATION NUMBER: US 08/487,429
 PRIOR FILING DATE: 1995-06-07
 PRIOR FILING DATE: 1995-04-21
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 1
 LENGTH: 1830121
 TYPE: DNA
 ORGANISM: Haemophilus influenzae
 FEATURE: misc feature
 NAME/KEY: misc feature
 LOCATION: (747)..(4747)
 OTHER INFORMATION: n equals a, t, g or c
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (921)..(921)
 OTHER INFORMATION: n equals a, t, g or c
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (10150)..(10150)
 OTHER INFORMATION: n equals a, t, g or c
 FEATURE:
 NAME/KEY: misc_feature

LOCATION: (29298)..(29298)
 OTHER INFORMATION: n equals a, t, g or c
 FEATURE: misc feature
 NAME/KEY: misc feature
 LOCATION: (36543)..(36543)
 OTHER INFORMATION: n equals a, t, g or c
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (36551)..(36551)
 OTHER INFORMATION: n equals a, t, g or c
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (36636)..(36636)
 OTHER INFORMATION: n equals a, t, g or c
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (40808)..(40810)
 OTHER INFORMATION: n equals a, t, g or c
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (4416)..(4416)
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Qy   1 GAGCTTGGAGCTCTGCTTACCACTGAGCTTACCCGC 42
Db   90995 GACCTTGGAGGTCTGCTTACCAACTGAGCTTACCCGC 90954

Search completed: January 10, 2006, 21:43:12
Job time : 836 secs

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us-10-645-818-5

GenCore version 5.1.6
 Copyright (c) 1993 - 2006 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 14:16:17 ; Search time 2184 Seconds

(without alignments)

1093.143 Million cell·updates/sec

Title: US-10-645-818-5

Perfect score: 42

Sequence: 1 gagttggaaatcgctgtct.....accaactggatccaccgc 42

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5883141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: gb_in;*
3: gb_env;*
4: gb_om;*
5: gb_ov;*
6: gb_pat;*
7: gb_ph;*
8: gb_pr;*
9: gb_ror;*
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11: gb_sy;*
12: gb_uni;*
13: gb_vir;*
14: gb_hcgc;*
15: gb_p1;*

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ALIGNMENTS

RESULT 1

AY297771 LOCUS Myxococcus xanthus strain D21 tRNA-Gly gene, and bacteriophage Mx9 DEFINITION attp2 site, complete sequence. ACCESSION AY297771 VERSION AY297771.1 GI:34329321 KEYWORDS Myxococcus xanthus SOURCE Myxococcus xanthus ORGANISM Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus. REFERENCE 1 (bases 1 to 360) AUTHORS Julien,B. TITLE Characterization of the integrase gene and attachment site for the Myxococcus xanthus bacteriophage Mx9 JOURNAL J. Bacteriol. 185 (21), 6325-6330 (2003) JOURNAL_PUBMED 14563867 REFERENCE 2 (bases 1 to 360) AUTHORS Julien,B.N. TITLE JOURNAL Hayward, CA 94545, USA LOCATION Submitted (13-MAY-2003) Koban Biosciences, 3832 Bay Center Place, Hayward, CA 94545, USA

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
1	42	100.0	AY297771	AY297771 Myxococcus AR619262 Sequence
2	42	100.0	4975	AR619262 Sequence
3	42	100.0	4981	AY24775 Bacterioid AE01629 Bacteroid
4	36.2	86.2	300162	AE01629 Bacteroid AE01714 Porphyrom AE01714 Porphyrom
5	36.2	86.2	30133	AE01714 Porphyrom AE01714 Porphyrom
c	6	34.6	82.4	9801788 Thermotog J01624 E.coli GLYW K01549 E.coli GLYW
c	7	32.4	77.1	J01624 E.coli GLYW K01549 E.coli GLYW
c	8	32.4	77.1	AR44940 Sequence X53236 E.coli GLYW
c	9	32.4	77.1	AR44940 Sequence X53236 E.coli GLYW
c	10	32.4	77.1	AY27RNAG3 AR657813 Synthetic AF274439 Pseudomon X52789 E.coli GLYW
c	11	32.4	77.1	AF274439 Pseudomon X52789 E.coli GLYW
c	12	32.4	77.1	X03239 E.coli GLYW M12299 E.coli pgs CQ872588 Sequence AJ004950 Pseudomon
c	13	32.4	77.1	X03239 E.coli GLYW M12299 E.coli pgs CQ872588 Sequence AJ004950 Pseudomon
c	14	32.4	77.1	6336 1 HMP1ATT AR657813 Synthetic AF274439 Pseudomon X52789 E.coli GLYW
c	15	32.4	77.1	6336 1 HMP1ATT AR657813 Synthetic AF274439 Pseudomon X52789 E.coli GLYW
c	16	32.4	77.1	596 1 ECOPGSA M12299 E.coli pgs
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Qy


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        Bacteroides thetaiotomicron VPI-5482
        Bacteroides thetaiotomicron VPI-5482
        Bacteroidetes; Bacteroidales (class); Bacteroidales;
        Bacteroidaceae; Bacteroides.
        1 (bases 1 to 300162)
Xu,J., Biursell,M.K., Himrod,J., Deng,S., Carmichael,L.K.,
Chiang,H.C., Hooper,L.V. and Gordon,J.I.
A Genomic View of the Human-Bacteroides thetaiotomicron Symbiosis
Science 299 (5615), 2074-2076 (2003)
12663928

2 (bases 1 to 300162)
Xu,J., Biursell,M.K., Himrod,J., Deng,S., Carmichael,L.K.,
Chiang,H.C., Hooper,L.V. and Gordon,J.I.
Direct Submission
Submitted (31-OCT-2002) Department of Molecular Biology and
Pharmacology, Washington University in St. Louis, 660 S. Euclid,
St. Louis, MO 63110, USA
12663928

FEATURES
  source
    AUTHORS
      AUTHORS
        Xu,J., Biursell,M.K., Himrod,J., Deng,S., Carmichael,L.K.,
        Chiang,H.C., Hooper,L.V. and Gordon,J.I.
        Direct Submission
        Submitted (31-OCT-2002) Department of Molecular Biology and
        Pharmacology, Washington University in St. Louis, 660 S. Euclid,
        St. Louis, MO 63110, USA
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Qy 2 AGCTTGGAAAGTCGTCGCTCACTGACCTACCCGC
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DEFINITION Porphyromonas gingivalis W83
ACCESSION AE017174 AB015924 AE017174.1 GI:34396675
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ORGANISM Porphyromonas gingivalis W83
Bacteria; Bacteroidetes (class); Bacteroidales;
Porphyromonadaceae; Porphyromonas.
REFERENCE 1 (bases 1 to 301933)
AUTHORS Nelson,K., Fleishmann,R., DeBoy,R., Paulsen,I., Pouts,D., Eisen,J.,
Daugherty,S., Dodson,R., Durkin,A., Gwinn,M., Haft,D., Kolonay,J.,
Neilson,W., White,O., Mason,T., Tallon,L., Gray,J., Granger,D.,
Tettelin,H., Dong,H., Galvin,J., Duncan,M., Dewhirst,F. and
Fraser,C.

TITLE Complete Genome Sequence of the Oral Pathogenic Bacterium
Porphyromonas gingivalis Strain W83
JOURNAL J. Bacteriol. 185 (18), 5591-5601 (2003)
PUBLMED 1249112
REFERENCE 2 (bases 1 to 301933)
AUTHORS Nelson,K., Fleishmann,R., DeBoy,R., Paulsen,I., Pouts,D., Eisen,J.,
Daugherty,S., Dodson,R., Durkin,A., Gwinn,M., Haft,D., Kolonay,J.,
Neilson,W., White,O., Mason,T., Tallon,L., Gray,J., Granger,D.,
Tettelin,H., Dong,H., Galvin,J., Duncan,M., Dewhirst,F. and
Fraser,C.

TITLE Direct Submission
JOURNAL Submitted (28-OCT-2002) The Institute for Genomic Research, 9712
FEATURES Medical Center Dr., Rockville, MD 20850, USA
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gene 5761 . 5877

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gene 7574 . 8476

CDS /locus tag="PG0556"

gene 7574 . 8476

/note="Identified by Glimmer2; putative"

codon_start=1 /transl_table=11

/product="hypothetical protein"

protein_id="AA065745.1"

/db_xref="GI: 34396680"

/translation="MMKKLSSCGVSSAVVNNGTIVQAGFLPAGTTRFTPMVLFQITSP
VTQGTYMAGMTKQMLNALEKDTLTFYTERMAKIKQSVSLINKNLKIFSDDLQ
QMKDHSLSLTIKNEFFEDLFLALIETKREVALAQSCEKEAKFTHME
LLEFLVWYLLTKTVELYMNRYIQDMNMRNWLNTFALIETSFDELLFMSMELINLHE
TVKKEFLLYEUSDLEGSPITFSKIRETKNSNFNSFTDIEEHNLLSEAKIHKSTLVR
FBKDMFVIDPRNGNIBLYSSNDQ"

gene 8531 . 9223

CDS /locus tag="PG0557"

gene 8531 . 9223

/note="Identified by Glimmer2; putative"

codon_start=1 /transl_table=11

/product="hypothetical protein"

protein_id="AA065746.1"

/db_xref="GI: 34396681"

/translation="MQLQRNNEVPIVKGRKLKSWNTAPRGFFGLFLVPLAATKQ
SLLNSLFLGMIWAVFIVLWLGVGTSSEYTKRKQIIMSDTAFLDOLHGTIHED
LYPEGGYEGSPERFPICPATEVKKTAGKIAEVYKSCYRSEASATMDREVMSGE
YNGDGHFHENCAVGFPKDWNPKDNPKANFALITFERBELLPTKNDWESTFGHSK
KAKDASRKNPOR"

complement(9755 . 10577)

gene 9223 . 9755

/note="putative"

codon_start=1 /transl_table=11

/product="hypothetical protein"

protein_id="AA065747.1"

/db_xref="GI: 34396682"

/translation="MPLQHNGVMSVTEHNGHPLNPLNPGVPMDFGRDPMTRVAY
DREFTAKAGAQELINIPIKEGVYVNGTSPSYTAEYFWGGOVGDATGMSMTVYEV
VARHTGIRYGMVSITNEGHFAODFVNDBQDVIRAANAASEKMGAIAPRLIAAV"

complement(10597 . 11742)

gene 9223 . 9755

CDS complement(10597 . 11742)

gene 9223 . 9755

/codon_start=1 /transl_table=11

/product="Purine nucleoside phosphorylase I, inosine and
guanosine-specific"

protein_id="AA065747.1"

/db_xref="GI: 34396682"

/translation="PMKLQSHYHRAAESLSSRLPDAKTAIIILSGSLGLBLAEKLENKT
VIPTNBIPHPAQATAVGHKGNIIIGLGGTPVAMQGRTHYEGYSMSQDVTFPVRMK
LGLIENFVNSAAGGQELNIPVKEGVYVNGTSPSYTAEYFWGGOVGDATGMSMTVYEV
VARHTGIRYGMVSITNEGHFAODFVNDBQDVIRAANAASEKMGAIAPRLIAAV"

complement(10597 . 11742)

gene 9223 . 9755

CDS /codon_start=1 /transl_table=11

/product="chlorohydroxylase family protein"

protein_id="AA065748.1"

/db_xref="GI: 34396683"

/translation="MAVIGLQNFQHNTSANTIFPGYGDOLRLMMWOLENTWIPVVAQMT
BEDVYWGSKIACLEMISCTTAFLDMDYMTLTAVARAVEEMGJRALVSLSTLFDRDQER
AIDERECLSHAEFCSKYSDIQPSVGPHTATVTSQEOQCHRFANEKRNLLHLS
BTTEGEVRDCLAKFGTTPVYRLKUGLISLGTGDCSSSNLNDIUMTAMKLAFLGKAWNSDAT
ASANMKLASEGRHYDEMRRKGIVIGLQHGTGDSQCSSENLLNDIUMTAMKLAFLGKAWNSDAT
AVAKATDIYSSATVDCARINGTDGTVAPRGLADCLRLDIPENTPCRNFIISLYVA
NSSAVDTIVDGKILMRGRKVPGBEALLGAAEAYKLMKAKAHCTE"

gene 11719 . 11964

CDS /locus tag="PG0560"

gene 11719 . 11964

/note="Identified by Glimmer2; putative"

codon_start=1 /transl_table=11

/product="hypothetical protein"

protein_id="AA065749.1"

/db_xref="GI: 34396684"

/translation="MQPGTNGHGRGIYNPIGMATRNRSLNHTVALDPDLTDTFQQC
LFYQYAQCSLMLKEGATGPFLYAPSTVSYLYMR"

gene 11719 . 11964

CDS complement(11946 . 13301)

gene 11719 . 11964

/note="Similar to GB: M9364, PID: 1033197, PID: 144480, and
SP: 059335; identified by sequence similarity; putative"

codon_start=1 /transl_table=11

/product="peptidase, M20/M25/M40 family"

protein_id="AA065750.1"

/db_xref="GI: 34396685"

/translation="MINIRDYTRNARFLDFAFLRISVSAEGBHPPDQMRCAEW
RDHHLQVGAQKAEVFOTPENPVYYAERIMDPKACTILVYAHYDMPPEPLWKSBEFP
BPHTRDGHFWARGADDKGQCMIQVKGPEPATAFLALGLVOCNCVKELPEGEEGISTNLEA
FCAKHEKMLSADVIIVSDTSMVSABTPSLTGLPHEVODVPUISDEEROMIAQVFSEKCYCOLDI
DTVPCGEAGSTLERNNSCRSPDVCGIAGGTYGEGAKTVPKAYKAVSSRLVANDQHE
KISONMFIDTIRSVAPKHKIVKTPLRHGGAYLCIDPLAKAAEACTIAFGKPLAV

Query Match	Score	Best Local Similarity	Length
Matches	86.2%	92.7%	301933;
Qy	2	90.0%; 0.011;	Conservative
Db	248859	0; Mismatches 3; Indels 0; Gaps 0;	DNA linear

BCT 04-JUN-2004
Thermotoga maritima MSB8 section 100 of 136 of the complete genome.

RESULT 6

AE001788 / C

LCUS DEFINITION AE001788 AE000512 ACCESSION

VERSION	AEO01788.1	GI:	4981893	
KEYWORDS	Thermotoga maritima MSB8			
ORGANISM	Bacteria; Thermotogae; Thermotogaceae; Thermotoga.	gene		
REFERENCE	1 (bases 1 to 9890)	CDS		
AUTHORS	Nelson, K.E., Clayton, R.A., Gill, S.R., Gwinn, M.L., Dodson, R.J., Haff, D.H., Hickie, J.D., Peterson, J.D., Nelson, W.C., Ketchum, K.A., McDonald, L., Utterback, T.R., Malek, J.A., Linher, K.D., Garrett, M.M., Stewart, A.M., Cotton, M.D., Pratt, M.S., Phillips, C.A., Richardson, D., Heidelberg, J., Sutton, J.G., Fleischmann, R.D., Eisen, J.A., White, O., Salzberg, S.L., Smith, H.O., Venter, J.C. and Fraser, C.M.			
TITLE	Evidence for lateral gene transfer between Archaea and bacteria from genome sequence of Thermotoga maritima			
JOURNAL	Nature 399 (6734), 323-329 (1999)			
PUBLISHER	1 (bases 1 to 9890)			
AUTHORS	Nelson, K.E., Clayton, R.A., Gill, S.R., Gwinn, M.L., Dodson, R.J., Haff, D.H., Hickie, J.D., Peterson, J.D., Nelson, W.C., Ketchum, K.A., McDonald, L., Utterback, T.R., Malek, J.A., Linher, K.D., Garrett, M.M., Stewart, A.M., Cotton, M.D., Pratt, M.S., Phillips, C.A., Richardson, D., Heidelberg, J., Sutton, J.G., Fleischmann, R.D., White, O., Salzberg, S.L., Smith, H.C., and Fraser, C.M.			
TITLE	Direct Submission (01-JUN-1999) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA	gene		
JOURNAL	Location/Qualifiers	CDS		
FEATURES	Source			
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	/strain="MSB8"			
	/db_xref="taxon:243274"			
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	/locus_tag="TM1334"			
	225..2009			
	/locus_tag="TM1334"			
	/note="similar to GB:AE000666 percent identity: 48.28; identified by sequence similarity; putative"			
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	/locus_tag="TM1335"			
	2002..3930			
	/locus_tag="TM1335"			
	/note="similar to percent identity: 0.00; identified by sequence similarity; putative"			
	/codon_start=1			
	/transl_table=11			
	/product="hypothetical protein"			
	/protein_id="AB16407.1"			
	/db_xref="GI:981895"			
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PRPLSAGKVINDRIOCPHGEPEKEPKFQDIDEDAYAFERLWNPFRAVENOLDWHLPPVHRIT
I1WDSGEGSEPERKEPKFQDIDEDAYAFERLWNPFRAVENOLDWHLPPVHRIT
IGRENRITLHGPKVYKWDSDSFITYFVNDPGRVKRVEKARSLRSVRYLTETIFPNL
WONHISCEQEDIRKDVLFQGDLPFLQKDFLRGGC"
RRVVTEQEDIRKDVLFQGDLPFLQKDFLRGGC"
7903. .876
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7903. .876
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sequence similarity; putative"
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PMLIYYSLWGLVLRGTVGYGTFFPKCPKFWYXVNVLVILPAFFQXQARLVEEV
DRFGVSLWGLVLRGTVGYGTFFPKCPKFWYXVNVLVILPAFFQXQARLVEEV
PSSWG"
8385. .894
gene
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sequence similarity; putative"
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/transl_table=11
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/db_xref="GI:4981902"
/translation="IMEWTRPLHVAASPEGPGCVAFLMTTISGFHIVVWQRQSMNMVFV
PIPHALLNQPLFWTGYSVPYLMR"
8647. .9036
gene
/locus_tag="TM1343"
/note="This region contains an authentic point mutation,
causing a premature stop, and is not the result of a
sequencing artifact. This region contains an authentic
frame shift and is not the result of a sequencing
artifact. similar to PID:1088462 PID:1848058"
complement(9194. .9267)
/locus_tag="tRNA-Met-1"
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/product="tRNA-Met"
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9373. .9445
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Query Match Similarity 82.4%; Score 34.6; DB 1; Length 9890;
Best Local Matches 90.2%; Prey No. 0.05%; Mismatches 0; Gaps 0;
Matches 37; Conservative 0; Indels 0;
tRNA
Query Match Similarity 82.4%; Score 34.6; DB 1; Length 9890;
Best Local Matches 90.2%; Prey No. 0.05%; Mismatches 0; Gaps 0;
Matches 37; Conservative 0; Indels 0;
Organism J01624.1
KeyWords GlyW gene; transfer RNA; transfer RNA-Gly.
Source Escherichia coli
Organism Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Reference 1 (bases 1 to 76)
RESULT 7
ECOGLYW/c ECOGLYW
LOCUS B. coli glyW gene, a duplicate gene for gly-tRNA-3, major species.
DEFINITION J01624
ACCESSION J01624.1
VERSION G1:146227
KEYWORDS GlyW gene; transfer RNA; transfer RNA-Gly.
SOURCE Escherichia coli
ORGANISM Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
REFERENCE 1 (bases 1 to 76)

```

AUTHORS	Tucker,S.D., Gopalakrishnan,A.S., Bollinger,R., Dowhan,W. and Murgola,E.J.
TITLE	Molecular mapping of glyW, a duplicate gene for tRNA ^{Gly} of Escherichia coli
JOURNAL	J. Bacteriol. 152 (2), 773-779 (1982)
PUBLMED COMMENT	Original source text: Escherichia coli DNA. PGSA [1]. The order of genes in this region is uvrC, pgA, glyW, fliA. Comparison of the order of determined restriction sites with the sites predicted from the nucleotide sequence of gly-tRNA indicates that the direction of transcription of glyW is counterclockwise on the circular E. coli map.
FEATURES	Location/Qualifiers 1..76 /organism="Escherichia coli" /mol_type="genomic DNA" /db_Xref="taxon:562" <1..>76 /product="tRNA-Gly" /note="gly-tRNA-3 [glyW]"
source	ORIGIN 10 bp upstream from Alu1 site; about 41.9 min on K12 map.
tRNA	Query Match 77.1%; Score 32.4; DB 1; Length 76; Best Local Similarity 85.7%; Bred. No. 0.59; Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 1
Qy	1 GAGCTTGGAGCTCGTCAACTGAGCTTACACCGC 42
Dg	42 GACCTTGCAAGTCGTCTTACCACTGCTATTCGCC 1
RESULT 8	
ECOTRG3/c	ECOTRG3 76 bp tRNA linear BCT 15-APR
LOCUS	E.coli Gly-tRNA-3 with mutation Gly-cRNA-ins.
DEFINITION	K01549
ACCESSION	K01549_1 GI:174426
VERSION	transfer RNA; transfer RNA-Gly.
KEYWORDS	Bscherichia coli
SOURCE	Bscherichia coli
ORGANISM	Bacteriia; Proteobacteria; Gammaproteobacteria; Enterobacteriia; Enterobacteriaceae; Escherichia.
REFERENCE	1 (bases 1 to 76)
AUTHORS	Squires,J.C. and Carbon,J.
TITLE	Natural and mutant glycine transfer RNAs
JOURNAL	Nature New Biol. 233 (43), 274-277 (1971)
PUBLMED COMMENT	Original source text: Escherichia coli tRNA. Contributed on tape April 1983 by M.Sprinzel & D.H.Gauss; from entry 0730 in Nucleic Acids Res. 11, R1-R54 (1983). Ins = insensitive to tryptone. The authors further suggest a model in which three copies of a gene specifying Gly-tRNA-3 exist in close proximity. These copies are suggested to be identical. [1] was unable to detect 4-thiouridine in either the wild-type or Gly-tRNA-ins, although a consistent low yield of Oligonucleotides containing 'U8' suggests that this base may be modified.
FEATURES	Location/Qualifiers 1..76 /organism="Escherichia coli" /mol_type="tRNA" /db_Xref="taxon:562" <1..>76 /product="tRNA-Gly" /note="codon recognized: GGC; Gly-tRNA-3 (NAR: 0730)"
source	
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modified_base	
modified_base	
modified_base	
variation	/note="g in wild-type; t in Gly-tRNA-ins"

/db_xref="GI:49081054"
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 "P
 misc_difference 185
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 misc_difference 478 .479
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ORIGIN

Query	Match	Score 77.1%; Best Local Similarity 85.7%; Matches 36; Conservative 0; Mismatches 0; Indels 6; Gaps 0;
Db	391	GACCTGGCAAGATCGTCTACCAACTGAGCTATTCCGGC 432

RESULT 12
 AP274339
LOCUS Pseudomonas syringae pv. glycinea thermoresponsive genetic locus, mutant PG180_617 sequence.
DEFINITION AF274339
VERSION AF274339.1 GI:11037462
KEYWORDS
ORGANISM Pseudomonas syringae pv. glycinea
 Pseudomonas syringae pv. glycinea
 Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 Pseudomonadaceae; Pseudomonas.

REFERENCE 1 (bases 1 to 490)
 Ullrich,M.S., Schergaut,M., Boch,J. and Ullrich,B.
TITLE Temperature-responsive genetic loci in the plant pathogen
 Pseudomonas syringae pv. glycinea
 Microbiology 146 (Pt 10), 2457-2468 (2000)
 2 (bases 1 to 490)
 Ullrich,M.S., Schergaut,M., Boch,J. and Ullrich,B.
REFERENCE Direct Submission
TITLE Submitted (02-JUN-2000) Ecophysiology, Max Planck Institute for
 Terrestrial Microbiology, Karl-von-Frisch-Straße, Marburg 35043,
 Germany

FEATURES
source
 Location/Qualifiers
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 /organism="Pseudomonas syringae pv. glycinea"
 /mol type="Genomic DNA"
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 /note="pathovar: glycinea"
misc_feature
 1..490
 /note="thermoreactive genetic locus, mutant PG4180.617;
 similar to Brunia chrysanthemi Ori possibly encoding a
 cyclase involved in polyketide synthesis"

ORIGIN

Query	Match	Score 77.1%; Best Local Similarity 85.7%; Matches 36; Conservative 0; Mismatches 0; Indels 6; Gaps 0;
Db	348	GACCTGGCAAGATCGTCTACCAACTGAGCTATTCCGGC 389

RESULT 13
 ECTRNGCL/c
LOCUS E.Coli GLY, cytB, and leuZ genes for tRNA-gly, tRNA-Cys and tRNA-Leu.
DEFINITION
ACCESSION X52789

VERSION X52789.1 GI:43166
KEYWORDS cyst gene; glw gene; leuZ gene; transfer RNA gene; transfer RNA-cys; transfer RNA-Gly; transfer RNA-Leu.
SOURCE Escherichia coli
ORGANISM Escherichia coli
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 Enterobacteriaceae; Escherichia.
REFERENCE Komine,Y., Adachi,T., Inokuchi,H. and Ozeki,H.
AUTHORS
TITLE Genomic organization and physical mapping of the transfer RNA genes in Escherichia coli K12
 J. Mol. Biol. 212 (4), 579-598 (1990)

JOURNAL J. Mol. Biol.
PUBMED 2184240
FEATURES
source
 Location/Qualifiers
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 /mol type="Genomic DNA"
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 /geno="glyW"
 /product="tRNA-Gly"
 /geno="cysT"
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 /geno="leuZ"
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 /product="tRNA-Leu"
ORIGIN

Query	Match	Score 77.1%; Best Local Similarity 85.7%; Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Db	156	GACCTGGCAAGATCGTCTACCAACTGAGCTATTCCGGC 115

RESULT 14
 HHPPIATT
LOCUS Haemophilus influenzae genes for tRNA-gly, tRNA-leu and tRNA-lys
DEFINITION and HPI host attachment site.
ACCESSION X53782
VERSION X53782.1 GI:43576
KEYWORDS bacteriophage attachment site; transfer RNA; transfer RNA-Lys;
SOURCE Haemophilus influenzae
ORGANISM Haemophilus influenzae
 Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 Pasteurellaceae; Haemophilus.
REFERENCE 1 (bases 1 to 636)
AUTHORS Hauser,M.A. and Scocca,J.J.
TITLE Location of the host attachment site for phage HPI within a cluster
 of Haemophilus influenzae tRNA genes
JOURNAL Nucleic Acids Res. 18 (17), 5305 (1990)
PUBMED 1698282
REFERENCE 2 (bases 1 to 636)
AUTHORS Scocca,J.J.
TITLE Direct Submission
JOURNAL Submitted (11-JUL-1990) Scocca,J.J., Dept. of Biochemistry, Johns
 Hopkins Univ., School of Hygiene, 615 N. Wolfe Street, Baltimore,
 MD 21205, USA
COMMENT Data kindly reviewed (08-OCT-1990) by Scocca J.
FEATURES

source 1. .636
 /organism="Haemophilus influenzae"
 /mol_type="genomic DNA"
 /strain="Rd001"
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 161. .342
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 complement(161. .236)
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 complement(287. .373)
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 330. .347
 /note="HPI attB sequence"
 complement(378. .453)
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 486
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 complement(494. .499)
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 complement(516. .521)
 /note="pot. -35 region"
 ORIGIN

Query Match Score 77.1%; Score 32.4%; DB 1; Length 636;
 Best Local Similarity 85.7%; Pred. No. 0 48;
 Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

repeat_unit 63. .68
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 repeat_unit 215. .220
 /note="imp. inverted repeat B"
 repeat_unit 227. .232
 /note="imp. inverted repeat B'"
 repeat_unit 456. .463
 /note="inverted repeat C"
 repeat_unit 468. .475
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 promoter 491. .496
 /note="pot. -35 sequence"
 promoter 514. .520
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 CDS 608. .838
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 /db_xref="GI:11605"
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 QEIPEQWLVAVWGGADYPRWASBKENTRA"

ORIGIN

Query Match Score 32.4%; DB 1; Length 890;
 Best Local Similarity 85.7%; Pred. No. 0 47;
 Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGCTTCGGAACTCGTGCTCTACCAACTGAGCTACCCGC 42
 Db 412 GACCTGGCAAGCTCGCTCACCCACTGAGCTACCCGC 453

ECGLYWG E. coli glyW region, a duplicated gene for tRNA-Gly-3. 890 bp DNA linear BCT 07-JUL-2002

RESULT 15
 ECGLYWG/C
 LOCUS X0339_1
 DEFINITION X0339_1 GI:1604
 ACCESSION X0339
 VERSION 1
 KEYWORDS insertion sequence; inverted repeat; transfer RNA-Gly; unidentified reading frame.

SOURCE Escherichia coli
 ORGANISM Escherichia coli
 Bacteria: Proteobacteria: Gammaproteobacteria: Enterobacteriales;
 Enterobacteriae; Escherichia.
 REFERENCE 1 (bases 110 to 185)
 AUTHORS Tucker,S.D., Gopalakrishnan,A.S., Bollinger,R., Dowhan,W. and Murgola,E.J.
 TITLE Molecular mapping of glyW, a duplicate gene for tRNA3Gly of Escherichia coli
 JOURNAL J. Bacteriol. 152 (2), 773-779 (1982)
 PUBMED 6298450
 PUBLISHER Tuckerman, S.D. and Murgola, E.J.
 REFERENCE 2 (bases 1 to 890)
 AUTHORS Tucker,S.D. and Murgola,E.J.
 TITLE Sequence analysis of the glyW region in Escherichia coli
 JOURNAL Biochimie 67 (9), 1053-1057 (1985)
 PUBMED 3005500
 COMMENT Data kindly reviewed (27-MAR-1986) by S. Tucker.
 FEATURES Location/Qualifiers
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 promoter 31..37
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 repeat_unit 53..57
 /note="imp. inverted repeat A"

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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 10:49:30 ; Search time 484 Seconds

(without alignments)

578.341 Million cell updates/sec

Title: US-10-645-818-5

Perfect score: 42

Sequence: 1 gagtttggaaatctcgatcgtat.....accaacttagtaccaccgc 42

Scoring table: IDENTITY_NUC

Gapop 10.0 . Gapext 1.0

Searched:

4996997 seqB, 332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

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- 1: N_Geneseq_21;*
- 2: geneseqn1990s;*
- 3: geneseqn2000s;*
- 4: geneseqn2001as;*
- 5: geneseqn2001bs;*
- 6: geneseqn2002as;*
- 7: geneseqn2002bs;*
- 8: geneseqn2003as;*
- 9: geneseqn2003bs;*
- 10: geneseqn2003cs;*
- 11: geneseqn2003ds;*
- 12: geneseqn2004as;*
- 13: geneseqn2004bs;*
- 14: geneseqn2005s;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

No.	Score	Match Length	DB ID	Description
c 1	42	100.0	42 12 Adm36323	Adm36323 Bacteriop
c 2	42	100.0	74 12 Adm36321	Adm36321 Myxococcu
c 3	42	100.0	257 12 Adm36309	Adm36309 Bacteriop
c 4	42	100.0	360 12 Adm36306	Adm36306 Bacteriop
c 5	42	100.0	360 12 Adm36307	Adm36307 Bacteriop
c 6	42	100.0	1647 12 Adm36304	Adm36304 Bacteriop
c 7	42	100.0	4575 14 Adm64194	Ac164194 M. xanthu
c 8	32.4	77.1	2558 12 Adm02418	Adl02418 DNA encod
c 9	32.4	77.1	549 11 Abd16247	Abd16247 Pseudomon
c 10	32.4	77.1	657 4 AAS51204	AAS51204 Salmonell
c 11	32.4	77.1	690 11 ABD16506	Abd16506 Pseudomon
c 12	32.4	77.1	1960 13 ADP05165	Adt05165 Haemophil
c 13	32.4	77.1	5436 13 ADP05456	Adt05456 Haemophil
c 14	32.4	77.1	5559 2 AAT05260	Aaq55260 Restricti
c 15	32.4	77.1	5559 2 AAT056101	Aat96101 Pseudomon
c 16	32.4	77.1	5559 2 AAT059212	Aat95212 5.6 kb E1
c 17	32.4	77.1	5559 2 AAT05945	Aat90945 E11 genom
c 18	32.4	77.1	5559 2 AAV06486	Aav06486 5.6 kb E1
c 19	32.4	77.1	10763 2 AAV39837	Aav39837 Pseudomon

ALIGNMENTS

RESULT 1	
ID	ADM36323 standard; DNA; 42 BP.
XX	
AC	ADM36323;
XX	
DT	03-JUN-2004 (first entry)
XX	
DE	Bacteriophage M9 int gene attP core site SEQ ID NO:5.
XX	
KW	bacteriophage; bacteriophage M9; integrase; enzyme; int gene;
KW	M9 transformation system; M9 integrase; molecular biology;
KW	drug development; attP; attachment site; gene; ds.
XX	
OS	Bacteriophage M9.
XX	
PN	WO200418635-A2.
XX	
PD	04-MAR-2004.
XX	
PP	20-AUG-2003; 2003WO-US026113.
XX	
PR	21-AUG-2002; 2002US-0405196P.
PA	(KOSA-) KOSAN BIOSCIENCES INC.
XX	
PJ	Julien B;
XX	
DR	WPI; 2004-226826/21.
XX	
PT	Modifying a DNA of a bacterial cell comprises using an integrase gene and an attachment site for <i>Myxococcus xanthus</i> bacteriophage Mx9, useful in the field of molecular biology and drug development.
XX	
PS	Claim 5; SEQ ID NO 5; 37pp; English.
XX	
CC	The present invention describes a method for modifying a DNA of a bacterial cell having in its genome a first attachment site recognised by a protein with Mx9 integrase activity comprising introducing an Mx9 transformation system into the cell, the system comprising a gene encoding a protein with Mx9 integrase activity operably linked to a promoter active in the host cell, and a DNA vector comprising a second

Qy 1 GAGCTTGGAAAGCTCTACCAACTGAGCTACCCACCGC 42
 DB 115 GAGCTTGGAAAGCTCTACCAACTGAGCTACCCACCGC 156

RESULT 4
 ID ADM36306 Standard; DNA; 360 BP.
 XX
 AC ADM36306;
 XX
 DR 03-JUN-2004 (first entry)
 XX
 DE Bacteriophage Mx9 integrase attB2 site nucleotide SEQ ID NO:4.
 XX
 DE Bacteriophage Mx9 integrase attB2 site nucleotide SEQ ID NO:4.
 XX
 DE bacterial; bacteriophage Mx9; integrase; enzyme; int gene;
 KW Mx9 transformation system; Mx9 integrase; molecular biology;
 KW drug development; attB2; gene; ds.
 XX
 OS Bacteriophage Mx9.
 XX
 PN WO2004018635-A2.

XX
 PD 04-MAR-2004.
 XX
 PF 20-AUG-2003; 2003WO-US026413.
 XX
 PR 21-AUG-2002; 2002US-0405196P.
 XX
 PA (KOSA-) KOSAN BIOSCIENCES INC.
 XX
 PI Julien B;
 XX
 PN WO2004018635-A2.
 XX
 DR 2004-226826/21.
 XX
 PT Modifying a DNA of a bacterial cell comprises using an integrase gene and
 PT an attachment site for Myxococcus xanthus bacteriophage Mx9, useful in
 PT the fields of molecular biology and drug development.
 XX
 PS Disclosure; SEQ ID NO 4; 37pp; English.

XX
 CC The present invention describes a method for modifying a DNA of a
 CC bacterial cell having in its genome a first attachment site recognised by
 CC a protein with Mx9 integrase activity comprises introducing an Mx9
 CC transformation system into the cell, the system comprising a gene
 CC encoding a protein with Mx9 integrase activity protein operably linked to
 CC a promoter active in the host cell, and a DNA vector comprising a second
 CC attachment site recognised by the integrase protein, which may be the
 CC same as the first attachment site. Also described is a bacterial host
 CC cell produced by the method described above. The methods and compositions
 CC of the present invention are useful in the fields of molecular biology
 CC and drug development, and particularly in transforming host bacterial
 CC cells using a bacteriophage Mx9 system. The present sequence represents a
 CC bacteriophage Mx9 int gene attB2 site nucleotide sequence, which is used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 360 BP; 68 A; 110 C; 124 G; 58 T; 0 U; 0 Other;

XX
 DR 2004-226826/21.
 XX
 PT Modifying a DNA of a bacterial cell comprises using an integrase gene and
 PT an attachment site for Myxococcus xanthus bacteriophage Mx9, useful in
 PT the fields of molecular biology and drug development.
 XX
 PS Disclosure; SEQ ID NO 3; 37pp; English.

XX
 CC The present invention describes a method for modifying a DNA of a
 CC bacterial cell having in its genome a first attachment site recognised by
 CC a protein with Mx9 integrase activity comprises introducing an Mx9
 CC transformation system into the cell, the system comprising a gene
 CC encoding a protein with Mx9 integrase activity protein operably linked to
 CC a promoter active in the host cell, and a DNA vector comprising a second
 CC attachment site recognised by the integrase protein, which may be the
 CC same as the first attachment site. Also described is a bacterial host
 CC cell produced by the method described above. The methods and compositions
 CC of the present invention are useful in the fields of molecular biology
 CC and drug development, and particularly in transforming host bacterial
 CC cells using a bacteriophage Mx9 system. The present sequence represents a
 CC bacteriophage Mx9 int gene attB1 site nucleotide sequence, which is used
 CC in the exemplification of the present invention.
 XX
 SQ Sequence 360 BP; 65 A; 104 C; 126 G; 65 T; 0 U; 0 Other;

Query Match 100.0%; Score 42; DB 12; Length 360;
 Best Local Similarity 100.0%; Pred. No. 3.7e-07;
 Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGCTTGGAAAGCTCTACCAACTGAGCTACCCACCGC 42
 DB 163 GAGCTTGGAAAGCTCTACCAACTGAGCTACCCACCGC 204

RESULT 5
 ID ADM36307 Standard; DNA; 360 BP.
 XX
 AC ADM36307;

The invention relates to an isolated nucleic acid encoding an *Moraxella catarrhialis* polypeptide. The nucleic acid is useful for preparing a composition for diagnosing, preventing or treating infection caused by *Moraxella catarrhialis*. The present sequence represents DNA encoding a *M. catarrhialis* protein.

Sequence 258 BP; 82 A; 57 C; 44 G; 75 T; 0 U; 0 Other;

Query Match 77.1%; Score 32.4; DB 11; Length 549;
Best Local Similarity 85.7%; Pred. No. 0.0036; Score 32.4; DB 11; Length 549;
Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX

Qy 1 GAGCTTGGAAAGCTCGTGTCTTACCAACTGAGCTACCCGC 42
Db 113 GACCTTGGCAAAGTCGCTTACCAACTGAGCTATCCGC 154

RESULT 9
ID ABD16247 Standard; DNA; 549 BP.

XX ABD16247;
XX DR 29-JUL-2004 (first entry)

XX DE Pseudomonas aeruginosa poly nucleotide #14851.

XX Bacterial infection; gene; ds; Pseudomonas aeruginosa infection;
KW antibacterial.
XX OS Pseudomonas aeruginosa.
XX PN US6551795-B1.
XX PR 22-APR-2003.
XX PD 18-FEB-1999;
XX PF 18-FEB-1998;
XX PR 27-JUL-1998;
XX PA (GENO-) GENOME THERAPEUTICS CORP.

XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX WPI; 2003-615309/58.
DR P-PSDB; AB082676.

XX Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* poly peptide, useful as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from bacterial infection.
PT Disclosure: SEQ ID NO 14851; 45pp; English.
XX The invention relates to *Pseudomonas aeruginosa* polypeptides and the polynucleotides encoding them. The sequences are useful in diagnosis and therapy of pathological conditions, as molecular targets for diagnostics, prophylaxis and treatment of pathological conditions resulting from a bacterial infection. For evaluating a compound, such as a polypeptide, for the ability to bind a *P. aeruginosa* nucleic acid, as components of effective antibacterial targets, as targets for antibacterial drugs, including anti-*P. aeruginosa* drugs, as templates for recombinant production of *P. aeruginosa*-derived peptides or polypeptides, as target components for diagnosis and/or treatment of *P. aeruginosa*-caused infection, and in detection of *P. aeruginosa* sequences or other sequences of *Pseudomonas* species using biotchip technology. Sequences AB01297-ABD17967 represent *P. aeruginosa* polynucleotides of the invention. Note: The sequence data for this patent did not form part of the printed specification but was obtained in electronic format from USPO at seqdata.uspto.gov/sequence.html.

CC Query Match 77.1%; Score 32.4; DB 4; Length 57;
CC Best Local Similarity 85.7%; Pred. No. 0.0037; Score 32.4; DB 4; Length 57;
CC Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
CC SQ Sequence 549 BP; 122 A; 166 C; 166 G; 95 T; 0 U; 0 Other;
CC XX SQ Sequence 549 BP; 122 A; 166 C; 166 G; 95 T; 0 U; 0 Other;

Query Match 77.1%; Score 32.4; DB 11; Length 549;
Best Local Similarity 85.7%; Pred. No. 0.0036; Score 32.4; DB 11; Length 549;
Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
XX Qy 1 GAGCTTGGAAAGCTCGTGTCTTACCAACTGAGCTACCCGC 42
Db 478 GACCTTGGCAAAGTCGCTTACCAACTGAGCTATCCGC 519
RESULT 10
ID AAS51204/C
ID AAS51204 Standard; DNA; 657 BP.
XX
Antisense; ss; prokaryotic cellular proliferation; antibiotic;
antibacterial; drug design.
XX DT 13-FEB-2002 (first entry)
XX DE Salmonella typhimurium cellular proliferation inhibitory sequence #102.
XX KW Salmonella typhimurium.
XX OS Salmonella typhimurium.
XX PN WO200170955-A2.
XX PD 27-SEP-2001.
XX PF 21-MAR-2001; 2001WO-US009180.
XX PR 21-MAR-2000; 2000US-01910178.
PR 23-MAY-2000; 2000US-0206648P.
PR 26-MAY-2000; 2000US-020772P.
PR 23-OCT-2000; 2000US-0242578P.
PR 27-NOV-2000; 2000US-0253625P.
PR 22-DEC-2000; 2000US-0257931P.
PR 16-FEB-2001; 2001US-0269308P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PT Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ;
PT PI Yamamoto RT, Xu HH;
XX DR WPI; 2001-611495/70.
XX PT New polynucleotides for the identification and development of antibiotics, comprise sequences of antisense nucleic acids.
XX PS Claim 1; SEQ ID NO 3781; 511pp; English.
XX The invention relates to antisense inhibitors of genes essential to prokaryotic cellular proliferation, their use in identifying the genes, their use in the discovery of novel antibiotics, the essential genes themselves and the encoded proteins. The prokaryotes used are *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhi*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The invention is also useful for the identification of potential new targets for antibiotic development. The antisense nucleic acids can also be used to identify these proteins, and to obtain antibodies capable of binding to the expressed proteins. The proteins can be used to screen compounds in rational drug discovery programmes. The antisense nucleic acid sequence is also useful to screen for homologous nucleic acids which are required for cell proliferation in a wide variety of organisms. The present sequence is an antisense oligonucleotide of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences

XX SQ Sequence 657 BP; 167 A; 140 C; 164 G; 183 T; 0 U; 3 Other;
XX SQ Sequence 549 BP; 122 A; 166 C; 166 G; 95 T; 0 U; 0 Other;

PA (CHIL-) CHILDRENS HOSPITAL INC.
 XX Bakaletz LO, Munson RS, Dyer DW;
 PI DR; WPI; 2004-662422/64.

XX New polynucleotides of nontypeable strain of *Haemophilus influenzae*,
 PT useful for treating or preventing *NTHi* bacterial infections of the middle
 PT ear and/or nasopharynx.

XX Example 1; SEQ ID NO 492; 88pp; English.

CC The invention comprises nucleotide sequences (genes) from the genome of a
 CC nontypeable strain of *Haemophilus influenzae* (*NTHi*). The *NTHi* DNA
 CC sequences of the invention are useful for treating or preventing *NTHi*
 CC bacterial infections of the middle ear and/or nasopharynx. The present
 CC nucleic acid represents an *NTHi* contig sequence of the invention.

XX Sequence 5436 BP; 1705 A; 1150 C; 884 G; 1691 T; 0 U; 6 Other;

Query Match 77.1%; Score 32.4; DB 13; Length 5436;
 Best Local Similarity 85.7%; Pred. No. 0.0061; DB 2;
 Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGCTTGGAAAGCTGCTTACCAACTGAGTACCGC 42
 Db 5153 GACCTTGGAAAGCTGCTTACCAACTGAGTATTCGGC 5112

RESULT 14
 AAQ55260 AAQ55260 standard; DNA; 5559 BP.
 XX AC AAQ55260;
 DT 25-MAR-2003 (revised)
 XX DE Restriction fragment comprising gene activating sequence.
 XX DE Gene activation; gafA; transcriptional activator; activator; sensor;
 KW regulation; induction; biocontrol agents; crop protection; ss.
 XX OS Pseudomonas fluorescens.

XX FH Key Location/Qualifiers
 FT CBS 210..1688
 FT /*tag= a
 FT /label= ORF 1.
 FT CBS 1906..3633
 FT /*tag= b
 FT /label= ORF 2.
 FT CBS 4616..4691
 FT /*tag= c
 FT /label= GlyW
 FT /note= "tRNA coding sequence."
 FT CDS 4731..5318
 FT /*tag= d
 FT /label= ORF 3.
 XX PN WO9401561-A1.
 XX PD 20-JAN-1994.
 XX PP 02-JUL-1993; 93WO-US006300.
 XX PR 02-JUL-1992; 92US-00908284.

PA (CIBA) CIBA GEIGY AG.
 XX PI Gaffney TD, Lam ST, Hill DS, Howell CR, Becker J;
 PI Ligon JM;

DR WPI; 1994-035057/04.
 XX PT Gene activating sequences, partic. from pseudomonas - used for inducing
 PT expression of genes which are latent or expressed at low levels in target
 PT organisms.
 XX PS Disclosure; Page 71-74; 87pp; English.
 CC The gene activating sequence is contained within an 11 kilobase EcoRI
 CC fragment (EII) from *P. fluorescens*. DNA sequence analysis of EII has
 CC identified five open reading frames (ORF), of which ORF and ORF 2 share
 CC significant homology with numerous activator and sensor components
 CC respectively of bacterial two-component regulatory systems. The gene
 CC activating sequences can be used in microorganisms to induce the
 CC production of gene products and secondary metabolites. They are used
 CC particularly for production of bacterial biocontrol agents for use in
 CC inhibiting plant pathogens. This sequence is a fragment of EII. See also
 CC AAQ55261. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 5559 BP; 1194 A; 1743 C; 1637 G; 984 T; 0 U; 1 Other;
 Query Match 77.1%; Score 32.4; DB 2; Length 5559;
 Best Local Similarity 85.7%; Pred. No. 0.0061;
 Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 Qy 1 GAGCTTGGAAAGCTGCTTACCAACTGAGTACCGC 42
 Db 4650 GACCTTGGAAAGCTGCTTACCAACTGAGTACCGC 4691

RESULT 15
 AAQ55260 AAQ55260 standard; DNA; 5559 BP.
 XX AC AAQ55260;
 DT 31-MAR-1998 (first entry)
 XX DE Pseudomonas fluorescens lemA gene fragment.
 XX KW lemA gene; gafA kinase; biocontrol factor; production; chitinase;
 KW gelatinase; pyrrolnitrin; cyanide; Pseudomonad; biological control;
 KW pathogenic fungus; ss.
 XX OS Pseudomonas fluorescens.
 XX PN US5686282-A.
 XX PD 11-NOV-1997.
 XX PP 02-JUN-1995; 95US-00459701.
 XX PR 20-AUG-1990; 90US-00570184.
 XX PR 02-JUL-1992; 92US-0090824.
 XX PR 01-JUL-1993; 93US-00087636.
 XX PR 08-JUN-1994; 94US-0025261.
 XX PR 08-AUG-1994; 94US-0028742.
 XX PA (NOVARTIS FINNANCE CORP.
 XX PI Lam ST, Gaffney TD;
 XX DR WPI; 1997-558141/51.
 XX PT Pseudomonas fluorescens lemA gene - useful for activating gene expression
 PT in Pseudomonads.
 XX PS Example 5; Col 41-45; 35pp; English.
 XX CC The present sequence is a Pseudomonas fluorescens lemA gene fragment. The
 CC P. fluorescens lemA gene, or lemA derivatives with enhanced gafA kinase
 CC activity, can be used to increase the product of biocontrol factors,
 CC e.g. chitinase, pyrrolnitrin and cyanide in Pseudomonads,

CC thus rendering them more effective for the biological control of
CC pathogenic fungi
XX
SQ Sequence 5559 BP; 1194 A; 1747 C; 1633 G; 984 T; 0 U; 1 Other;
Query Match 77.1%; Score 32.4; DB 2; Length 5559;
Best Local Similarity 85.7%; Prod. No. 0.0061;
Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 GAGCTTGGAAAGTCGTCGTACCAACTGAGCTACCGC 42
Db 4650 GACCTTGGCAAGTCGTCGTACCAACTGAGCTATCCGC 4691

Search Completed: January 10, 2006, 17:45:34
Job time : 487 secs

us-10-645-818-5.rst

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 10, 2006, 16:47:24 ; Search time 3793 Seconds

(without alignments)

518.075 Million cell updates/sec

Title: US-10-645-818-5

Perfect score: 42

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Scoring table: IDENTITY_NNC

Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database :

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  2: gb_est2:*
  3: gb_est3:*
  4: gb_htc:*
  5: gb_est4:*
  6: gb_est5:*
  7: gb_est6:*
  8: gb_est7:*
  9: gb_gb1:*
 10: gb_gb2:*
 11: gb_gb3:*
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RESULT 1

CL688860/c

LCUS

DEFINITION

PRI014c_BR (760) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic survey sequence.

ACCESSION

CL688860

VERSION

GI:50197938

KEYWORDS

GSS,

SOURCE

Pristionchus pacificus

ORGANISM

Pristionchus pacificus

Bukaryota; Metazoa;

Neodiplogasteridae;

Pristionchus.

SUMMARIES

Query

Match

Length

DB

ID

Description

Result No.	Score	Query Length	DB ID	Description
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c 2	32.4	77.1	773	CL692030 PRI0158a_F
c 3	32.4	77.1	782	BZ564906 pacb2-164
c 4	32.4	77.1	805	BZ551245 pacb1-50
c 5	32.4	77.1	811	CL664382 PRI0146a_F
c 6	32.4	77.1	1250	BZ563705 pacb2-164
c 7	32.4	77.1	1333	BZ57553 mah2_5462
c 8	32.4	77.1	1615	BZ575755 mah2_4612
c 9	30.8	73.3	556	CN692030 B0352G09_F
c 10	30.8	73.3	665	BU702632 UI-M-FCO-
c 11	30.8	73.3	680	CF725482 UI-M-G00-
c 12	30.8	73.3	719	CR320878 UI-M-FR0-
c 13	30.8	73.3	729	CF732833 UI-M-G70-
c 14	29.8	71.0	427	AL390454 Leishmani
c 15	29.8	71.0	503	BB430019 TA006_B0
c 16	28.8	68.6	922	BH163135 ENTTB3TF
c 17	28.2	67.1	696	BH371106 AG-ND-175
c 18	27.6	65.7	692	AG391506 Mus muscu
c 19	27.2	64.8	606	CX06239 BHAGP5TR
c 20	27.2	64.8	708	CC822117 MBSPI2B8
c 21	26.8	63.8	180	AZ608686 IM0433L04
c 22	26.8	63.8	312	AZ945284 2M0206B2

FEATURES

source

Location/Qualifiers

1..760

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/mol type="genomic DNA"

/strain="California"

/db_xref="taxon:54126"

/clone lib="Mixed stage fosmid library of P. pacificus

var. "California"

/note="Vector: pEpifos-5 Fosmid vector"

ORIGIN

Query Match

Score 32.4 ; DB 10 ;

Pred. No. 0.088 ;

Matches 36 ;

Conservative 0 ;

Indels 0 ;

Gaps 0 ;

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBLMED
 COMMENT

Contact: Sommer RJ

Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 07071601371
 Fax: 00497071601498
 Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
 AppDB: an AceDB database for the nematode satellite organism
 Pristionchus pacificus
 Nucleic Acids Res. 32 (1), D421-D422 (2004)

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBLMED
 COMMENT

Evolutionary Biology
 Max-Planck-Institute for Developmental Biology
 Spemannstr. 37-39, Tuebingen D-72076, Germany
 Tel: 07071601371
 Fax: 00497071601498
 Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
 This library was generated at Caitech, Pasadena, USA and end sequenced at Vancouver, Canada.
 Seq Primer: T7
 Class: fosmid ends.

Location/Qualifiers

1..760

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/mol type="genomic DNA"

/strain="California"

/db_xref="taxon:54126"

/clone lib="Mixed stage fosmid library of P. pacificus

var. "California"

/note="Vector: pEpifos-5 Fosmid vector"

Query Match

Score 32.4 ; DB 10 ;

Best Local Similarity 85.7% ; Pred. No. 0.088 ;

Matches 36 ; Conservative 0 ; Indels 0 ; Gaps 0 ;

Length 760 ;

Qy	1 GAGCTTGGAAACTCGTCCTACCACTGAGTACCCGC 42 259 GACCTGGCAAGTCGCTTACCACTGAGTACCCGC 218	COMMENT	Contact: Chris K. Raymond Genome Center University of Washington Box 352445, Seattle, WA 98105-2145, USA
RESULT 2 CL69230/c	CL69230 DNA linear GSS 10-JUL-2004 PR1158a_A12_2 - PR10158a_BR (773) Mixed stage fosmid library of <i>P. pacificus</i> var. California <i>Pristionchus pacificus</i> genomic, genomic sequence. CL69230 CL69230_1 GI:50213938	FEATURES Source	FEATURES Source /organism="Pseudomonas aeruginosa" /mol_type="genomic DNA" /strain="2-164" /db_xref="taxon:287" /clone="pac82-164" /clone_lib="pac82-164" /note="clincical isolate 2-164 Whole genomic shotgun library."
DEFINITION VERSION KEYWORDS ORGANISM REFERENCE AUTHORS TITLE JOURNAL PUBLMED COMMENT	Pristionchus pacificus Neodiplogasteridae; Pristionchidae; Diplogasterida; Eukaryota; Metazoa; Nematoda; Chromadorea; Diplogasterida; Neodiplogasteridae; Pristionchidae; Pristionchus. 1 (bases 1 to 773) AppDB: An AceDB database for the nematode satellite organism <i>Pristionchus pacificus</i> Nucleic Acids Res. 32 (1), D421-D422 (2004) Contact: Sommer RJ Evolutionary Biology Max-Planck-Institute for Developmental Biology Spemannstr. 37-39, Tuebingen D-72076, Germany Tel: 00497071601371 Fax: 00497071601498 Email: ralf.sommer@tuebingen.mpg.de This library was generated at Caltech, Pasadena, USA and end sequenced at Vancouver, Canada. Seq primer: T7 Class: fosmid ends.	FEATURES Source	FEATURES Source /organism="Pristionchus pacificus" /mol_type="genomic DNA" /strain="California" /db_xref="taxon:54126" /clone lib="Mixed stage fosmid library of <i>P. pacificus</i> var. "California" /note="Vector: pEPfob5 Fosmid vector"
LOCUS DEFINITION VERSION KEYWORDS ORGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT	GSS 10-JUL-2004 PR1158a_A12_2 - PR10158a_BR (773) Mixed stage fosmid library of <i>P. pacificus</i> var. California <i>Pristionchus pacificus</i> genomic, genomic sequence. CL69230 CL69230_1 GI:50213938	FEATURES Source	FEATURES Source /organism="Pseudomonas aeruginosa" /mol_type="genomic DNA" /strain="2-164" /db_xref="taxon:287" /clone="pac82-164" /clone_lib="pac82-164" /note="clincical isolate 2-164 Whole genomic shotgun library."
RESULT 3 BZ564906/c	BZ564906 DNA linear GSS 17-DEC-2002 pacc2-164_4981-x1 pacc2-164 Pseudomonas aeruginosa genomic clone. BZ564906 BZ564906_1 GI:27191664	FEATURES Source	FEATURES Source /organism="Pseudomonas aeruginosa" /mol_type="genomic DNA" /strain="1-60" /db_xref="taxon:287" /clone="pac81-60" /clone_lib="pac81-3056" /note="clincical isolate 1-60 Whole genomic shotgun library."
DEFINITION VERSION KEYWORDS ORGANISM REFERENCE AUTHORS TITLE JOURNAL	pacc2-164_4981, genomic survey sequence. Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas. Spencer,D.H., Raymond,C.K., Smith,E.B., Sims,E.E., Hastings,M., Burns,J.L., Kaul,R. and Olsen,M.V. Whole-Genome-Sequence variation among multiple isolates of <i>Pseudomonas aeruginosa</i> library J. Bacteriol. (2002) In press	FEATURES Source	FEATURES Source /organism="Pseudomonas aeruginosa" /mol_type="genomic DNA" /strain="1-60" /db_xref="taxon:287" /clone="pac81-60" /clone_lib="pac81-3056" /note="clincical isolate 1-60 Whole genomic shotgun library."

Db 384 GACCTGGCAAAGTCGCTCACCAACTGAGCTATCCGGC 343

RESULT 5

LOCUS CL664382 c 811 bp DNA linear GSS 09-JUL-2004
DEFINITION PRI0146d_G08 - PRI0146d_B21 (811) Mixed stage fosmid library of P.
pacificus var. California *Pristionchus pacificus* genomic, genomic
survey sequence.

ACCESSION CL664382
VERSION CL664382.1 GI:50154798
KEYWORDS
SOURCE
ORGANISM *Pristionchus pacificus*
Pristionchus pacificus Eukaryota; Meazoa; Nemata; Chromadorea; Diplogasterida;
Neodiplogasteridae; *Pristionchus*.
1 (bases 1 to 811) Srinivasan, J., Otto, G.W., Kahlow, U., Geisler, R., and Sommer, R.J.
TITLE AppDB: an AccDB database for the nematode satellite organism
Pristionchus pacificus
JOURNAL Nucleic Acids Res. 32 (1), D421-D422 (2004)
PUBLISHED 14661447
COMMENT Contact: Sommer, R.J.
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq Primer: T7
Class: Fosmid ends.

FEATURES Source
LOCUS BZ563705
DEFINITION pac82-164_4385.y2_pacs2_164_Pseudomonas aeruginosa genomic clone
pac82-164_4385_y2_genomic survey sequence.

ACCESSION BZ563705
VERSION BZ563705.1 GI:27188137
KEYWORDS
SOURCE
ORGANISM *Pseudomonas aeruginosa*
Pseudomonas aeruginosa Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; *Pseudomonas*.
1 (bases 1 to 1393) Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R., and Olsen, M.V.
TITLE Whole-Genome Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
JOURNAL COMMENT Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216554
Fax: 2066857244
Email: craymond@u.washington.edu

FEATURES Source
LOCUS BZ563705
DEFINITION pac82-164_4385.y2_pacs2_164_Pseudomonas aeruginosa genomic clone
pac82-164_4385_y2_genomic survey sequence.

ACCESSION BZ563705
VERSION BZ563705.1 GI:27188137
KEYWORDS
SOURCE
ORGANISM *Pseudomonas aeruginosa*
Pseudomonas aeruginosa Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; *Pseudomonas*.
1 (bases 1 to 1250) Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R., and Olsen, M.V.
TITLE Whole-Genome Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
JOURNAL COMMENT Contact: Chris K. Raymond
Genome Center

University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216554
Fax: 2066857244
Email: craymond@u.washington.edu

FEATURES Source
LOCUS BZ577553
DEFINITION msh2_5462_x1_msh_Pseudomonas aeruginosa genomic clone msh2_5462,
genomic survey sequence.

ACCESSION BZ577553
VERSION BZ577553.1 GI:2712614
KEYWORDS GSS,
ORGANISM *Pseudomonas aeruginosa*
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; *Pseudomonas*.
1 (bases 1 to 1393) Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R., and Olsen, M.V.
TITLE Whole-Genome Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
JOURNAL COMMENT Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216554
Fax: 2066857244
Email: craymond@u.washington.edu

FEATURES Source
LOCUS BZ577553
DEFINITION msh2_5462_x1_msh_Pseudomonas aeruginosa genomic clone msh2_5462,
genomic survey sequence.

ACCESSION BZ577553
VERSION BZ577553.1 GI:2712614
KEYWORDS GSS,
ORGANISM *Pseudomonas aeruginosa*
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; *Pseudomonas*.
1 (bases 1 to 1393) Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R., and Olsen, M.V.
TITLE Whole-Genome Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
JOURNAL COMMENT Contact: Chris K. Raymond
Genome Center

RESULT 6

LOCUS BZ563705/c 1250 bp DNA linear GSS 17-DEC-2002
DEFINITION pac82-164_4385.y2_pacs2_164_Pseudomonas aeruginosa genomic clone
pac82-164_4385_y2_genomic survey sequence.

ACCESSION BZ563705
VERSION BZ563705.1 GI:27188137
KEYWORDS
SOURCE
ORGANISM *Pseudomonas aeruginosa*
Pseudomonas aeruginosa Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; *Pseudomonas*.
1 (bases 1 to 1250) Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R., and Olsen, M.V.
TITLE Whole-Genome Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
JOURNAL COMMENT Contact: Chris K. Raymond
Genome Center

Query Match Score 32.4; DB 9; Length 1393;
Best Local Similarity 85.7%; Pred. No. 0.094;
Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGCTTGGAAAGCTCGTCTACCAACTGAGCTTACCCGC 42
Db 706 GACCTTGGCAAGTCGCTCACCAACTGAGCTTACCCGC 665

ORIGIN

RESULT	8	BZ575755	1635 bp	DNA	linear	GSS 17-DEC-2002								
LOCUS		BZ575755	msh2_4612-x1	msh Pseudomonas aeruginosa	genomic clone	msh2_4612,								
DEFINITION			genomic survey sequence.											
ACCESSION		BZ575755												
KEYWORDS		GSS												
SOURCE		Pseudomonas aeruginosa												
ORGANISM		Pseudomonas aeruginosa	Bacteria; Probeobacteria; Gammaproteobacteria; Pseudomonadales;	Pseudomonadaeae; Pseudomonas.										
REFERENCE		Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M., Burns, J.L., Kaul, R. and Olsen, M.V.												
AUTHORS			Whole-Genome-sequence variation among multiple isolates of Pseudomonas aeruginosa library											
TITLE			J. Bacteriol. (2002) In press											
JOURNAL			Contact: Chris K. Raymond											
COMMENT			Genome Center											
FEATURES	source	University of Washington Box 352145, Seattle, WA 98105-2145, USA Tel: 206/216944 Fax: 066857244 Email: raymond@u.washington.edu Class: shotgun												
FEATURES	source	1. 1635 /organism="Pseudomonas aeruginosa" /mol_type="genomic DNA" /strain="MSH"												
FEATURES	source	/db_xref="taxon:287" /clone="msh2_4612" /clone_id="msh" /note="Environmental isolate. Whole genomic shotgun library."												
ORIGIN			Query Match Score 77.1%; Best Local Similarity 85.7%; Matches 36; Conservative 0; Mismatches 6; Indels 0; Gaps 0;											
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RESULT	9	CN694592	556 bp	mRNA	linear	EST 18-MAY-2004								
LOCUS		B0352G09-5	NIA Mouse El0.5 whole embryo cDNA library (Long)	Mus musculus	clone NIA:B0352G09 IMAGE:3:0863984 5', mRNA sequence.									
DEFINITION														
ACCESSION		CN694592												
VERSION		CN694592.1												
KEYWORDS		EST: Mus musculus (house mouse)												
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Scirurognathi; Muroidea; Muridae; Murinae; Mus.												
REFERENCE		I bases 1 to 556) Sharov, A.A., Piao, Y., Matoba, R., Dukekula, D.B., Qian, Y.,'U.C., Vanhaugen, V., Falco, G., Martin, P.R., Stagg, C.A., Bassay, U.C., Wang, Y., Carter, M.G., Hamatani, T., Aiba, K., Akutsu, H., Sharova, L., Tanaka, T.S., Kimber, W.L., Yoshioka, T., Jaradat, S.A., Pantano, S., Nagraja, R., Boheler, K.R., Taub, D., Hodges, R.J., Longo, D.L., Schlessinger, D., Keller, J.J., Klotz, E., Kelsoe, G., Umehara, A., Vesco, A.L., Rossant, J., Kunath, T., Hogan, B.L., Curci, A., D'Urso, M., Kelsso, J., Hide, W. and Ko, M.S.												
AUTHORS		Transcriptome analysis of mouse stem cells and early embryos PLOS Biol. 1 (3), 410-419 (2003)												
JOURNAL		Contact: Dawood B. Dukekula												
COMMENT														

Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cawseall Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@gsu.nih.gov
plate: B0352 row: G column: 09
Seq primer: M13 Reverse
High quality sequence stop: 556
POLYA=No.

FEATURES source Location/Qualifiers 1. .556 /organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="niasstr: B0352G09-5" /clone: NIA:B0352G09 IMAGE:3:0863984 " /tissue type="whole embryo including extraembryonic tissues at 10.5-days postcoitum" /dev_stage="E10.5" /lab_host="DH10B" /clone.lib="NIA Mouse E10.5 whole embryo cDNA library (Long)" /note="Vector: pCMV-SPORTS (Invitrogen); Site 1: SalI; Site 2: NotI; Mouse cDNA project by the Laboratory of GeneFics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://igsu.gsc.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544189]). Total RNAs were extracted from a pool of 8 embryos at 10.5-days postcoitum. Double stranded cDNAs were synthesized with an Oligo(dT) primer (Invitrogen) 5'-PGACTAGTCATGATTCGCGCCCTTTTTTTTTT-3' from 2ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol precipitation. The cDNAs were ligated to Lone-linker LL-SalI, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Tag polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centrificon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORTS plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.4Kb. The library was constructed by Yulan Piao."

FEATURES source Location/Qualifiers 1. 1635 /organism="Pseudomonas aeruginosa" /mol_type="genomic DNA" /strain="MSH"

FEATURES source /db_xref="taxon:287" /clone="msh2_4612" /clone_id="msh" /note="Environmental isolate. Whole genomic shotgun library."

ORIGIN Query Match Score 73.3%; Best Local Similarity 83.3%; Matches 35; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

ORIGIN Query Match Score 30.8%; Best Local Similarity 83.3%; Matches 35; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

RESULT 10 BUT02692 LOCUS UI-M-FCO-bzb-P-24-0-UI.r1 NIH_BvAP_FCO_Mus_musculus_CDNA_clone DEFINITION IMAGE:6:01543 5', mRNA sequence.

ACCESSION BUT02692 VERSION BUT02692.1 SOURCE EST. ORGANISM Mus musculus (house mouse) Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Scirurognathi; Muroidea; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 665) NIH_MGC http://mgc.nci.nih.gov/. AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC) TITLE Unpublished (1999) JOURNAL

COMMENT	
Contact: Robert Strausberg, Ph.D. Email: cgabbs@mail.nih.gov	
Tissue Procurement: Dr. James Lin, University of Iowa CDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov	
This clone was contributed by the Brain Molecular Anatomy Project (BMAP)	
The following repetitive elements were found in this cDNA sequence: 7-103, >PB1D0#STRP/Alu (matched compliment) 45-185, >B4#S1NB/B4 (matched compliment)	
Seq primer: PYX-5	
FEATURES	source
Location/Qualifiers	
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/clone="IMAGE:6401543"	
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/lab_host="DH10B (T1 phage resistant)"	
/clone_id="NIH_BMAP_PCO"	
/note="Organ: brain; Vector: PYX-Asc; Site 1: EcoR I; Site 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured mRNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I, and then cloned directionally into PYX-Asc vector. The library tag sequence located between the Not I site and the polytail is TGAGAGGCC. This library was created for the University of Iowa Mouse Brain Molecular Anatomy Project (BMAP); Gene Discovery in the Developing Mouse Nervous System', supported by National Institutes of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."	
ORIGIN	
Query Match 73.3%; Score 30.8; DB 5; Length 665;	
Best Local Similarity 83.3%; Pred. No. 0.37;	
Matches 35; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
Dy 1 GAGCTGGAGCTCTGTCTACCAACTGAGCTAACCGC 42	
Db 139 GTGCTTGGAGGCAAGCGCTCTACCAACTGAGCTAACCCCTC 180	
RESULT 11	
CP725482 680 bp mRNA linear EST 09-OCT-2003	
UI-M-GZ0-cjm-c-18-0-UT.r1 NIH_BMAP_GZ0 Mus musculus CDNA clone IMAGE:10603233 5 , mRNA sequence.	
DEFINITION	
Mammalia; Eutheria; Burchontoglires; Gliridae; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
ACCESSION	
CF725482.1 GI:37599650	
ORGANISM	
Mus musculus (house mouse)	
VERSION	
EST.	
KEYWORDS	
ORGANISM	
Mus musculus	
REFERENCE	
NIH-MGC http://mgc.ncbi.nlm.nih.gov/	
AUTHORS	
National Institutes of Health, Mammalian Gene Collection (MGC)	
TITLE	
Unpublished (1999)	
JOURNAL	
Contact: Robert Strausberg, Ph.D.	
Email: cgabbs@mail.nih.gov	
COMMENT	
CDDA Library Preparation: Dr. James Lin, University of Iowa	
CDNA Library Preparation: Dr. James Lin, University of Iowa	

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/mousefl.html>
 This clone was contributed by the Brain Molecular Anatomy Project
 (BMAP).

The following repetitive elements were found in this CDNA sequence: 1-116, >ORF1#DNA-MER1 type 300-412, >B1_MMHSINE/Alu (matched compliment) 346-442, >PB1D0#SINE/Alu (mached compliment) 384-524, >B4#SINE/B4 (mached compliment)

Seq primer: pX-5.

Location/Qualifiers

1. .660 source

FEATURES

1. /organism="Mus musculus"
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 /db_xref="Taxon:10030"
 /clone="IMAGE:10603133"
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 /dev_stage="embryo 12.5-13.5-14.5 dpc"
 /lab_host="DH10B (T1 phage resistant)"
 /clone_id="NIH_BMAP_GZ0"
 /note="Organ: Eye; Vector: pX- ABC; Site 1: EcoR I;
 Site 2: Not I; The library was constructed according to BonaIdo, Lennon and Soars, Genome Research, 6:79-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with Not I and then cloned directionally into pX-ABC vector. The library tag sequence located between the Not I site and the poly A tail is TTTTGAGT. This library was created for the University Iowa Brain Anatomy Project (BIAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemir Chin, Ph.D., program coordinator."

http://image.llnl.gov	This clone was contributed by the Brain Molecular Anatomy Project (BMAP). The following repetitive elements were found in this sequence: 26-166, >LINE#LINE/L1 (matched compliment) Seq primer: PYX-5.	FEATURES	source	FEATURES	source
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	/strain="IC57BL/6"			/strain="IC57BL/6"	
	/db_xref="taxon:10090"			/db_xref="taxon:10090"	
	/clone="IMAGE:1617273"			/clone="IMAGE:1617273"	
	/tissue_type="whole brain"			/tissue_type="whole brain"	
	/dev_stage="embryo:13.5-14.5-16.5-17.5dpfc"			/dev_stage="embryo:13.5-14.5-16.5-17.5dpfc"	
	/lab_host="DRI:OB (T1 phage resistant)"			/lab_host="DRI:OB (T1 phage resistant)"	
	/clone_lib="NTH_BMAP_FW0"			/clone_lib="NTH_BMAP_G20"	
	/note="Organ: Brain; Vector: PYX- ASC; Site:1: ECOR I; Site:2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with Not I and then cloned directionally into PYX-ASC vector. The library tag sequence located between the Not I site and the polyA tail is TTAATGAGCT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."			/note="Organ: Eye; Vector: PYX- ASC; Site: 1: ECOR I; Site: 2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with Ecor I adaptor, digested with Not I and then cloned directionally into PYX-ASC vector. The library tag sequence located between the Not I site and the polyA tail is TTAATGAGCT. This library was created for the University Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."	
	ORIGIN			ORIGIN	
	Query Match Score 73.3%; Best Local Similarity 83.3%; Matches 35; Conservative 0; Mismatches 0; Gaps 0;			Query Match Score 73.3%; Best Local Similarity 83.3%; Matches 35; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
Qy	1 GAGCTGGAAACTCTCGTCCTACCAACTGAGCTTACCCGC 42			Qy 1 GAGCTGGAAACTCTCGTCCTACCAACTGAGCTTACCCGC 42	
Db	120 GTGCTGGAACTCAACCTGACTGCTAACCTGACTGCTAACCCCTC 161			Db 566 GTGCTGGAACTCAACCTGACTGCTAACCCCTC 607	
	RESULT 13			RESULT 14	
	LOCUS CF732823			P862R/C	
	DEFINITION CF732823			LOCUS P862R	
	ACCESSION UI-N-GZ0-cjlr-0-12-0-UI			DEFINITION Leishmania major Friedlin PAC P862 right	
	IMAGE:306003899 5'			ACCESSION survey sequence.	
	KEYWORDS mRNA			IMAGE AL1390545	
	SOURCE Mus musculus (house mouse)			KEYWORDS GI:9501521	
	ORGANISM Mus musculus			SOURCE GSS	
	TITLE NIH MGC http://mgc.ncbi.nih.gov/			ORGANISM Leishmania major	
	JOURNAL Unpublished (1999)			KEYWORDS Eukaryota; Kinetoplastida; Trypanosomatidae; Leishmania.	
	COMMENT Contact: Robert Strausberg Ph.D. Email: cgabbs-r@mail.nih.gov			REFERENCE 1 (bases 1 to 427)	
	Tissue Procurement: Dr. James Lin University of Iowa cDNA Library preparation: Dr. M. Bento Soares, University of Iowa DNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/mousefl1.html This clone was contributed by the Brain Molecular Anatomy Project (BMAP).			AUTHORS Ivens,A.C., Lewis,S.M., Bagherzadeh,A., Zhang,L., Chan,H.M. and Smith,D.F.	
	The following repetitive elements were found in this sequence: 1-33, >PBD9#SINE/Alu (matched compliment) 43-204, >URR1B#DNA/MER1_Type 388-530, >Bl_MM#SINE/Alu (matched compliment)			TITLE A physical map of the Leishmania major Friedlin genome	
				JOURNAL Genome Res. 8 (2), 135-145 (1998)	
				COMMENT Direct Submission Submitted (24-JUL-2000) Leishmania major Friedlin genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA, E-mail: barrel@sanger.ac.uk and alcat@sanger.ac.uk	
				REFERENCE see http://www.ebi.ac.uk/parasites/leish.html Details of Leishmania sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/L.major/	
				AUTHORS Taylor,R.G., Huckie,E.B.J., Ivens,A.C., Rajandream,M.A. and Barrell,B.G.	
				TITLE JOURNAL	
				REFERENCE 2 (bases 1 to 427)	
				AUTHORS Taylor,R.G., Huckie,E.B.J., Ivens,A.C., Rajandream,M.A. and Barrell,B.G.	
				COMMENT FEATURES source	
				The primer sequence can be obtained from alcat@sanger.ac.uk.	
				1. .427 Location/Qualifiers /organism="Leishmania major"	

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/mol type="genomic DNA"
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/clone="PAC P862"

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ORIGIN

Qy	2	AGCTTGGAAAGCTGTCGTCATCAACTGAGGTACCCGC 42
Db	322	ACCTTGGCAAGTTGCGCTCATCAACTGAGGTACCCGC 282

RESULT 15

BE430009/c	BE430009	503 bp mRNA Linear EST 26-JUL-2000
LOCUS	TAS006.B02R990616	ESTC TAS Wheat cDNA Library <i>Triticum aestivum</i>
DEFINITION	CDNA clone TAS006.B02.	mRNA sequence.
ACCESSION	BE430009	
KEYWORDS	BB427852	
SOURCE	Triticum aestivum (bread wheat)	
ORGANISM	Triticum aestivum	
PREFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Poaceae;	
AUTHORS	Pooidae; Triticeae; <i>Triticum</i> , Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Herrmann, R.G., Holton, T., Jacquin, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pechioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M., and Wenzel, G.	
TITLE	International Triticeae EST Cooperative (ITREC): Production of Expressed Sequence Tags for Species of the Triticeae Unpublished (2000)	
JOURNAL	Contact: Selvaraj G Plant Biotechnology Institute, National Research Council of Canada 110 Gymnasium Place, Saskatoon, SK S7N 0W9 Canada Tel: 306 975 5577 Fax: 306 975 4839 Email: Gopalan.Selvaraj@nrc.ca International Triticeae EST Cooperative (ITREC) http://wheat.pw.usda.gov/Genome/	
COMMENT	1..503	
FEATURES	/organism="Triticum aestivum" source /mol type="mRNA" /db_xref="taxon:4565" /clone="TAS006.B02" /clone_lib="ITREC TAS Wheat cDNA Library"	
ORIGIN	Query Match Score 29.8; DB 11; Length 427; Best Local Similarity 82.9%; Pred. No. 0.86; Matches 34; Conservative 0; Mismatches 7; Indels 0; Gaps 0;	
Qy	2	AGCTTGGAAAGCTGTCGTCATCAACTGAGGTACCCGC 42
Db	369	ACCTTGGCAAGTTGCGCTCATCAACTGAGGTACCCGC 329

Search completed: January 10, 2006, 19:25:38
Job time : 3798 secs

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